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(54) Title: **PROBES AND DECODER OLIGONUCLEOTIDES**

(57) Abstract: The present invention is directed to improved methods and compositions for the use of adapter sequences on arrays in a variety of multiplexed nucleic acid reactions, including synthesis reactions, amplification reactions, and genotyping reactions.

**WO 02/16649 A2**

## PROBES AND DECODER OLIGONUCLEOTIDES

This application claims the benefit of U.S.S.N.s 60/227,948 filed August 25, 2000 and 60/228,854, filed August 29, 2001, both of which are expressly incorporated herein by reference.

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### FIELD OF THE INVENTION

The present invention is directed to methods and compositions for the use of adapter sequences on arrays in a variety of nucleic acid reactions, including synthesis reactions, amplification reactions, and genotyping reactions.

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### BACKGROUND OF THE INVENTION

The detection of specific nucleic acids is an important tool for diagnostic medicine and molecular biology research. Gene probe assays currently play roles in identifying infectious organisms such as bacteria and viruses, in probing the expression of normal and mutant genes and identifying mutant genes such as oncogenes, in typing tissue for compatibility preceding tissue transplantation, in matching tissue or blood samples for forensic medicine, and for exploring homology among genes from different species.

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Ideally, a gene probe assay should be sensitive, specific and easily automatable (for a review, see Nickerson, Current Opinion in Biotechnology 4:48-51 (1993)). The requirement for sensitivity (i.e. low detection limits) has been greatly alleviated by the development of the polymerase chain reaction (PCR) and other amplification technologies which allow researchers to amplify exponentially a specific nucleic acid sequence before analysis (for a review, see Abramson et al., Current Opinion in Biotechnology, 4:41-47 (1993)).

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Specificity, in contrast, remains a problem in many currently available gene probe assays. The extent of molecular complementarity between probe and target defines the specificity of the interaction. Variations in the concentrations of probes, of targets and of salts in the hybridization medium, in the reaction temperature, and in the length of the probe may alter or influence the specificity of the

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probe/target interaction.

It may be possible under some circumstances to distinguish targets with perfect complementarity from targets with mismatches, although this is generally very difficult using traditional technology, since small variations in the reaction conditions will alter the hybridization. New experimental techniques for mismatch detection with standard probes include DNA ligation assays where single point mismatches prevent ligation and probe digestion assays in which mismatches create sites for probe cleavage.

Recent focus has been on the analysis of the relationship between genetic variation and phenotype by making use of polymorphic DNA markers. Previous work utilized short tandem repeats (STRs) as polymorphic positional markers; however, recent focus is on the use of single nucleotide polymorphisms (SNPs), which occur at an average frequency of more than 1 per kilobase in human genomic DNA. Some SNPs, particularly those in and around coding sequences, are likely to be the direct cause of therapeutically relevant phenotypic variants and/or disease predisposition. There are a number of well known polymorphisms that cause clinically important phenotypes; for example, the apoE2/3/4 variants are associated with different relative risk of Alzheimer's and other diseases (see Cordor et al., Science 261(1993). Multiplex PCR amplification of SNP loci with subsequent hybridization to oligonucleotide arrays has been shown to be an accurate and reliable method of simultaneously genotyping at least hundreds of SNPs; see Wang et al., Science, 280:1077 (1998); see also Schafer et al., Nature Biotechnology 16:33-39 (1998). The compositions of the present invention may easily be substituted for the arrays of the prior art.

There are a variety of particular techniques that are used to detect sequence, including mutations and SNPs. These include, but are not limited to, ligation based assays, cleavage based assays (mismatch and invasive cleavage such as Invader™), single base extension methods (see WO 92/15712, EP 0 371 437 B1, EP 0317 074 B1; Pastinen et al., Genome Res. 7:606-614 (1997); Syvänen, Clinica Chimica Acta 226:225-236 (1994); and WO 91/13075), and competitive probe analysis (e.g. competitive sequencing by hybridization; see below).

Oligonucleotide ligation amplification ("OLA", which is referred as the ligation chain reaction (LCR) when two-stranded reactions or nested reactions are done) involves the ligation of two smaller probes into a single long probe, using the target sequence as the template. See generally U.S. Patent Nos. 5,185,243, 5,679,524 and 5,573,907; EP 0 320 308 B1; EP 0 336 731 B1; EP 0 439 182 B1; WO 90/01069; WO 89/12696; WO 97/31256 and WO 89/09835, all of which are incorporated by reference.

Invasive cleavage technology is based on structure-specific nucleases that cleave nucleic acids in a site-specific manner. Two probes are used: an "invader" probe and a "signalling" probe, that adjacently hybridize to a target sequence with a non-complementary overlap. The enzyme cleaves at the overlap due to its recognition of the "tail", and releases the "tail" with a label. This can then be

detected. The Invader™ technology is described in U.S. Patent Nos. 5,846,717; 5,614,402; 5,719,028; 5,541,311; and 5,843,669, all of which are hereby incorporated by reference.

5 An additional technique utilizes sequencing by hybridization. For example, sequencing by hybridization has been described (Drmanac et al., Genomics 4:114 (1989); Koster et al., Nature Biotechnology 14:1123 (1996); U.S. Patent Nos. 5,525,464; 5,202,231 and 5,695,940, among others, all of which are hereby expressly incorporated by reference in their entirety).

10 Sensitivity, i.e. detection limits, remain a significant obstacle in nucleic acid detection systems, and a variety of techniques have been developed to address this issue. Briefly, these techniques can be classified as either target amplification or signal amplification. Target amplification involves the amplification (i.e. replication) of the target sequence to be detected, resulting in a significant increase in the number of target molecules. Target amplification strategies include the polymerase chain reaction (PCR), strand displacement amplification (SDA), and nucleic acid sequence based  
15 amplification (NASBA).

Alternatively, rather than amplify the target, alternate techniques use the target as a template to replicate a signalling probe, allowing a small number of target molecules to result in a large number of signalling probes, that then can be detected. Signal amplification strategies include the ligase chain  
20 reaction (LCR), cycling probe technology (CPT), invasive cleavage techniques such as Invader™ technology, Q-Beta replicase (Q $\beta$ R) technology, and the use of "amplification probes" such as "branched DNA" that result in multiple label probes binding to a single target sequence.

The polymerase chain reaction (PCR) is widely used and described, and involves the use of primer  
25 extension combined with thermal cycling to amplify a target sequence; see U.S. Patent Nos. 4,683,195 and 4,683,202, and PCR Essential Data, J. W. Wiley & sons, Ed. C.R. Newton, 1995, all of which are incorporated by reference. In addition, there are a number of variations of PCR which also find use in the invention, including "quantitative competitive PCR" or "QC-PCR", "arbitrarily primed PCR" or "AP-PCR", "immuno-PCR", "Alu-PCR", "PCR single strand conformational polymorphism" or "PCR-SSCP", allelic PCR (see Newton et al. Nucl. Acid Res. 17:2503 91989); "reverse transcriptase PCR" or  
30 "RT-PCR", "biotin capture PCR", "vectorette PCR", "panhandle PCR", and "PCR select cDNA subtraction", among others.

Strand displacement amplification (SDA) is generally described in Walker et al., in Molecular Methods  
35 for Virus Detection, Academic Press, Inc., 1995, and U.S. Patent Nos. 5,455,166 and 5,130,238, all of which are hereby incorporated by reference.

Nucleic acid sequence based amplification (NASBA) is generally described in U.S. Patent No. 5,409,818 and "Profiting from Gene-based Diagnostics", CTB International Publishing Inc., N.J., 1996,



both of which are incorporated by reference.

Cycling probe technology (CPT) is a nucleic acid detection system based on signal or probe amplification rather than target amplification, such as is done in polymerase chain reactions (PCR).

5 Cycling probe technology relies on a molar excess of labeled probe which contains a scissile linkage of RNA. Upon hybridization of the probe to the target, the resulting hybrid contains a portion of RNA:DNA. This area of RNA:DNA duplex is recognized by RNaseH and the RNA is excised, resulting in cleavage of the probe. The probe now consists of two smaller sequences which may be released, thus leaving the target intact for repeated rounds of the reaction. The unreacted probe is removed and  
10 the label is then detected. CPT is generally described in U.S. Patent Nos. 5,011,769, 5,403,711, 5,660,988, and 4,876,187, and PCT published applications WO 95/05480, WO 95/1416, and WO 95/00667, all of which are specifically incorporated herein by reference.

The oligonucleotide ligation assay (OLA) involve the ligation of at least two smaller probes into a single  
15 long probe, using the target sequence as the template for the lgase. See generally U.S. Patent Nos. 5,185,243, 5,679,524 and 5,573,907; EP 0 320 308 B1; EP 0 336 731 B1; EP 0 439 182 B1; WO 90/01069; WO 89/12696; and WO 89/09835, all of which are incorporated by reference.

Invader™ technology is based on structure-specific polymerases that cleave nucleic acids in a site-specific manner. Two probes are used: an "invader" probe and a "signalling" probe, that adjacently  
20 hybridize to a target sequence with overlap. For mismatch discrimination, the invader technology relies on complementarity at the overlap position where cleavage occurs. The enzyme cleaves at the overlap, and releases the "tail" which may or may not be labeled. This can then be detected. The Invader™ technology is described in U.S. Patent Nos. 5,846,717; 5,614,402; 5,719,028; 5,541,311; and 5,843,689, all of which are hereby incorporated by reference.  
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"Branched DNA" signal amplification relies on the synthesis of branched nucleic acids, containing a multiplicity of nucleic acid "arms" that function to increase the amount of label that can be put onto one probe. This technology is generally described in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730,  
30 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference.

Similarly, dendrimers of nucleic acids serve to vastly increase the amount of label that can be added to a single molecule, using a similar idea but different compositions. This technology is as described  
35 in U.S. Patent No. 5,175,270 and Nilsen et al., J. Theor. Biol. 187:273 (1997), both of which are incorporated herein by reference.

U.S.S.N.s 09/189,543; 08/944,850; 09/033,462; 09/287,573; 09/151,877; 09/187,289 and 09/256,943; and PCT applications US98/09163 and US99/14387; US98/21193; US99/04473 and US98/05025, all

of which are expressly incorporated by reference, describe novel compositions utilizing substrates with microsphere arrays, which allow for novel detection methods of nucleic acid hybridization.

The use of adapter-type sequences that allow the use of universal arrays has been described in limited contexts; see for example Chee et al., Nucl. Acid Res. 19:3301 (1991); Shoemaker et al., Nature Genetics 14:450 (1996); U.S. Patent Nos. 5,494,810, 5,830,711, 6,027,889, 6,054,564, and 6,268,148; and EP 0 799 897 A1; WO 97/31256, all of which are expressly incorporated by reference.

Accordingly, it is an object of the present invention to provide methods for detecting nucleic acid reactions, and other target analytes, on arrays using adapter sequences.

#### SUMMARY OF THE INVENTION

In accordance with the above objects, the invention also provides a method of detecting a target nucleic acid. The method comprises contacting the target nucleic acid with an adapter sequence such that the target nucleic acid is joined to the adapter sequence to form a modified target nucleic acid. In addition, the method comprises contacting the modified target nucleic acid with an array comprising a substrate with a surface comprising discrete sites and a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that the first capture probe and the modified target nucleic acid form a complex, wherein the microspheres are distributed on the surface, and detecting the presence of the target nucleic acid. In addition the method comprises adding at least one decoding binding ligand to the array such that the identity of the target nucleic acid is determined. Preferably the adapter nucleic acids include a sequence as set forth in Table I, Table II, Table III or Table IV.

In addition the invention provides a method of making an array. The method comprises forming a surface comprising individual sites on a substrate, distributing microspheres on the surface such that the individual sites contain microspheres, wherein the microspheres comprise at least a first and a second subpopulation each comprising a capture probe, wherein the capture probe is complementary to an adapter sequence, the adapter sequence joined to a target nucleic acid, and an identifier binding ligand that will bind at least one decoder binding ligand such that the identification of the target nucleic acid is elucidated. Preferably the adapter nucleic acids include a sequence as set forth in Table I, Table II, Table III or Table IV.

In addition the invention provides a kit comprising at least one nucleic acid selected from the group consisting of the sequences set forth in Table I, Table II, Table III or Table IV. In one embodiment the invention provides a kit that includes a nucleic acid that includes a sequence as set forth in Table I, Table II, Table III or Table IV and at least a first universal priming sequence.

In addition the invention includes an array composition comprising a first population of microspheres comprising first and second subpopulations, wherein the first subpopulation includes a first nucleic acid selected from the sequences set forth in Table I, Table II, Table III or Table IV and the second subpopulation includes a second sequence selected from the sequences set forth in Table I, Table II, Table III or Table IV.

In addition the invention includes an array composition comprising a first sequence at a known location on a substrate, wherein the first sequence is selected from the sequences set forth in Table I, Table II, Table III or Table IV.

In addition the invention includes a method for making an array. The method includes distributing a population of microspheres on an substrate, wherein the population includes first and second subpopulations, wherein the first subpopulation includes a first sequence selected from the group consisting of the sequences set forth in Table I, Table II, Table III or Table IV and the second subpopulation includes a second sequence selected from the group consisting of the sequences set forth in Table I, Table II, Table III or Table IV.

In addition the method includes a method of immobilizing a target nucleic acid. The method includes hybridizing a first adapter probe with a first target nucleic acid, wherein the first adapter probe comprises a first domain that is complementary to the first target nucleic acid and a second domain, comprising a first sequence selected from the sequences set forth in Table I, Table II, Table III or Table IV to form a first hybridization complex. In addition the method includes contacting the first hybridization complex with a first capture probe immobilized on a first substrate, wherein the first capture probe is substantially complementary to the second domain of the first adapter probe.

In addition the invention includes a method of decoding an array composition comprising providing an array composition that includes a substrate with a surface comprising discrete sites and a population of microspheres comprising at least a first and a second subpopulation, wherein each subpopulation comprises a bioactive agent. The microspheres are distributed on the surface. The method further includes adding a plurality of decoding binding ligands to the array composition to identify the location of at least a plurality of the bioactive agents wherein at least a first decoder binding ligand comprises a sequence selected from the group consisting of the sequences of Table I, Table II, Table III or Table IV.

A method of detecting a target nucleic acid sequence, said method comprising attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein the first adapter nucleic acid includes a sequence selected from the sequences set forth in Table I, Table II, Table III or Table IV. The method further includes contacting the modified first target nucleic acid sequence with an array comprising a substrate with a patterned surface

comprising discrete sites and a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that the first capture probe and the modified first target nucleic acid sequence form a hybridization complex; wherein the microspheres are distributed on the surface and detecting the presence of the modified first target nucleic acid sequence.

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#### DETAILED DESCRIPTION OF THE FIGURES

Figure 1 depicts a method of selecting oligonucleotide sequences.

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Figure 2 depicts a scheme for selection of probes and decoder oligonucleotides.

Figure 3 demonstrates hybridization intensity comparison of immobilized beads using non-purified oligonucleotides with HPLC purified oligonucleotides.

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Figure 4 depicts different oligonucleotide sequences immobilized onto silica beads at various salt concentration. Average intensity indicates hybridization intensity of beads in a BeadArray.

Figure 5 depicts immobilization of oligonucleotides in increasing salt concentrations.

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#### DETAILED DESCRIPTION OF THE INVENTION

This invention is directed to the use of adapter sequences, and optionally capture extender probes, that allow the use of "universal" arrays. That is, a "universal" array is an array with a set of capture probes that will hybridize to adapter sequences, for use in any number of different reactions, including the binding of nucleic acid reactions and other target analytes comprising a nucleic acid adapter sequence that can hybridize to the array. In this way, a manufacturer of arrays can make one type of array that may be used in a variety of applications, thus reducing the manufacturing costs associated with the array. In addition, in the case of bead arrays, the decoding steps as outlined below can be simplified, as one set of decoding probes can be made.

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In general, the use of adapter sequences can be described as follows for nucleic acid reactions. An adapter sequence can be added exogenously to a target nucleic acid sequence using any number of different techniques, including, but not limited to, amplification reactions as described in U.S.S.N. 09/425,633, filed October 22, 1999; 09/513,362, filed February 25, 2000; 09/517,945, filed March 3, 2000; 09/535,854, filed March 27, 2000; 09/553,993, filed April 20, 2000; 09/556,463, filed April 21, 2000; 60/135,051, filed May 20, 1999; 60/135,053, filed May 20, 1999; 60/135,123, filed May 20, 1999; 60/130,089, filed April 20, 1999; 60/160,917, filed October 22, 1999; 60/160,927, filed October 22,

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1999; 60/161,148, filed October 22, 1999; and 60/244,119, filed October 26, 2000 all of which are hereby incorporated by reference. In addition, the adapter can be added to an extension probe. The adapter sequence can then be used to target to its complementary capture probe on the surface.

- 5 Alternatively, the adapter sequences can be added to other target analytes, to generate unique and reproducible arrays of target analytes in a similar manner. By adding the nucleic acid to the target analyte (for example to an antibody in an immunoassay), the target analytes may then be arrayed.

10 Accordingly, the present invention provides methods for the detection of target analytes, particularly nucleic acid target sequences, in a sample. As will be appreciated by those in the art, the sample solution may comprise any number of things, including, but not limited to, bodily fluids (including, but not limited to, blood, urine, serum, lymph, saliva, anal and vaginal secretions, perspiration and semen, of virtually any organism, with mammalian samples being preferred and human samples being particularly preferred); environmental samples (including, but not limited to, air, agricultural, water and  
15 soil samples); biological warfare agent samples; research samples; purified samples, such as purified genomic DNA, RNA, proteins, etc.; raw samples (bacteria, virus, genomic DNA, etc.; As will be appreciated by those in the art, virtually any experimental manipulation may have been done on the sample.

20 The present invention provides methods for the detection of target analytes, particularly nucleic acid target sequences, in a sample. By "target analyte" or "analyte" or grammatical equivalents herein is meant any molecule, compound or particle to be detected. As outlined below, target analytes preferably bind to binding ligands, as is more fully described below. As will be appreciated by those in the art, a large number of analytes may be detected using the present methods; basically, any target  
25 analyte for which a binding ligand, described below, may be made may be detected using the methods of the invention.

Suitable analytes include organic and inorganic molecules, including biomolecules. In a preferred embodiment, the analyte may be an environmental pollutant (including pesticides, insecticides, toxins, etc.); a chemical (including solvents, polymers, organic materials, etc.); therapeutic molecules  
30 (including therapeutic and abused drugs, antibiotics, etc.); biomolecules (including hormones, cytokines, proteins, lipids, carbohydrates, cellular membrane antigens and receptors (neural, hormonal, nutrient, and cell surface receptors) or their ligands, etc); whole cells (including procaryotic (such as pathogenic bacteria) and eukaryotic cells, including mammalian tumor cells); viruses  
35 (including retroviruses, herpesviruses, adenoviruses, lentiviruses, etc.); and spores; etc. Particularly preferred analytes are environmental pollutants; nucleic acids; proteins (including enzymes, antibodies, antigens, growth factors, cytokines, etc); therapeutic and abused drugs; cells; and viruses.

In a preferred embodiment, the target analyte is a protein. As will be appreciated by those in the art,

there are a large number of possible proteinaceous target analytes that may be detected using the present invention. By "proteins" or grammatical equivalents herein is meant proteins, oligopeptides and peptides, derivatives and analogs, including proteins containing non-naturally occurring amino acids and amino acid analogs, and peptidomimetic structures. The side chains may be in either the (R) or the (S) configuration. In a preferred embodiment, the amino acids are in the (S) or L-configuration. As discussed below, when the protein is used as a binding ligand, it may be desirable to utilize protein analogs to retard degradation by sample contaminants.

Suitable protein target analytes include, but are not limited to, (1) immunoglobulins, particularly IgEs, IgGs and IgMs, and particularly therapeutically or diagnostically relevant antibodies, including but not limited to, for example, antibodies to human albumin, apolipoproteins (including apolipoprotein E), human chorionic gonadotropin, cortisol,  $\alpha$ -fetoprotein, thyroxin, thyroid stimulating hormone (TSH), antithrombin, antibodies to pharmaceuticals (including antiepileptic drugs (phenytoin, primidone, carbamazepine, ethosuximide, valproic acid, and phenobarbital), cardioactive drugs (digoxin, lidocaine, procainamide, and disopyramide), bronchodilators (theophylline), antibiotics (chloramphenicol, sulfonamides), antidepressants, immunosuppressants, abused drugs (amphetamine, methamphetamine, cannabinoids, cocaine and opiates) and antibodies to any number of viruses (including orthomyxoviruses, (e.g. Influenza virus), paramyxoviruses (e.g. respiratory syncytial virus, mumps virus, measles virus), adenoviruses, rhinoviruses, coronaviruses, reoviruses, togaviruses (e.g. rubella virus), parvoviruses, poxviruses (e.g. variola virus, vaccinia virus), enteroviruses (e.g. poliovirus, coxsackievirus), hepatitis viruses (including A, B and C), herpesviruses (e.g. Herpes simplex virus, varicella-zoster virus, cytomegalovirus, Epstein-Barr virus), rotaviruses, Norwalk viruses, hantavirus, arenavirus, rhabdovirus (e.g. rabies virus), retroviruses (including HIV, HTLV-I and -II), papovaviruses (e.g. papillomavirus), polyomaviruses, and picomaviruses, and the like), and bacteria (including a wide variety of pathogenic and non-pathogenic prokaryotes of interest including *Bacillus*; *Vibrio*, e.g. *V. cholerae*; *Escherichia*, e.g. Enterotoxigenic *E. coli*, *Shigella*, e.g. *S. dysenteriae*; *Salmonella*, e.g. *S. typhi*; *Mycobacterium* e.g. *M. tuberculosis*, *M. leprae*; *Clostridium*, e.g. *C. botulinum*, *C. tetani*, *C. difficile*, *C. perfringens*; *Corynebacterium*, e.g. *C. diphtheriae*; *Streptococcus*, *S. pyogenes*, *S. pneumoniae*; *Staphylococcus*, e.g. *S. aureus*; *Haemophilus*, e.g. *H. influenzae*; *Neisseria*, e.g. *N. meningitidis*, *N. gonorrhoeae*; *Yersinia*, e.g. *Y. pestis*, *Pseudomonas*, e.g. *P. aeruginosa*, *P. putida*; *Chlamydia*, e.g. *C. trachomatis*; *Bordetella*, e.g. *B. pertussis*; *Treponema*, e.g. *T. pallidum*; and the like); (2) enzymes (and other proteins), including but not limited to, enzymes used as indicators of or treatment for heart disease, including creatine kinase, lactate dehydrogenase, aspartate amino transferase, troponin T, myoglobin, fibrinogen, cholesterol, triglycerides, thrombin, tissue plasminogen activator (tPA); pancreatic disease indicators including amylase, lipase, chymotrypsin and trypsin; liver function enzymes and proteins including cholinesterase, bilirubin, and alkaline phosphatase; aldolase, prostatic acid phosphatase, terminal deoxynucleotidyl transferase, and bacterial and viral enzymes such as HIV protease; (3) hormones and cytokines (many of which serve as ligands for cellular receptors) such as erythropoietin (EPO), thrombopoietin (TPO), the interleukins

(including IL-1 through IL-17), insulin, insulin-like growth factors (including IGF-1 and -2), epidermal growth factor (EGF), transforming growth factors (including TGF- $\alpha$  and TGF- $\beta$ ), human growth hormone, transferrin, epidermal growth factor (EGF), low density lipoprotein, high density lipoprotein, leptin, VEGF, PDGF, ciliary neurotrophic factor, prolactin, adrenocorticotrophic hormone (ACTH),  
5 calcitonin, human chorionic gonadotropin, cortisol, estradiol, follicle stimulating hormone (FSH), thyroid-stimulating hormone (TSH), luteinizing hormone (LH), progesterone, testosterone, ; and (4) other proteins (including  $\alpha$ -fetoprotein, carcinoembryonic antigen CEA.

10 In addition, any of the biomolecules for which antibodies may be detected may be detected directly as well; that is, detection of virus or bacterial cells, therapeutic and abused drugs, etc., may be done directly.

15 Suitable target analytes include carbohydrates, including but not limited to, markers for breast cancer (CA15-3, CA 549, CA 27.29), mucin-like carcinoma associated antigen (MCA), ovarian cancer (CA125), pancreatic cancer (DE-PAN-2), and colorectal and pancreatic cancer (CA 19, CA 50, CA242).

20 In a preferred embodiment, the target analyte (and various adapters and other probes of the invention), comprise nucleic acids. By "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., Tetrahedron 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzl et al., Eur. J. Biochem. 81:579 (1977); Letsinger et al., Nucl.  
25 Acids Res. 14:3487 (1986); Sawai et al, Chem. Lett. 805 (1984), Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); and Pauwels et al., Chemica Scripta 26:141 (1986)), phosphorothioate (Mag et al., Nucleic Acids Res. 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., J. Am. Chem. Soc. 111:2321 (1989), O-methylphosphoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., Chem. Int. Ed. Engl. 31:1008 (1992); Nielsen, Nature, 365:566 (1993); Carlsson et al., Nature 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowski et al., Angew. Chem. Intl. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al.,  
35 Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Lett. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) and non-ribose backbones, including those described in U.S.

Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within the definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done to facilitate the addition of labels, alter the hybridization properties of the nucleic acids, or to increase the stability and half-life of such molecules in physiological environments.

As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made. Alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature ( $T_m$ ) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in  $T_m$  for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. This allows for better detection of mismatches. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribonucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. A preferred embodiment utilizes isocytosine and isoguanine in nucleic acids designed to be complementary to other probes, rather than target sequences, as this reduces non-specific hybridization, as is generally described in U.S. Patent No. 5,681,702. As used herein, the term "nucleoside" includes nucleotides as well as nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

In general, probes of the present invention (including adapter sequences and capture probes, described below) are designed to be complementary to a target sequence (either the target sequence of the sample or to other probe sequences, for example adapter sequences) such that hybridization of the target and the probes of the present invention occurs. This complementarity need not be perfect;



there may be any number of base pair mismatches that will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by

5 "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under the selected reaction conditions.

When nucleic acids are to be detected, they are referred to herein as "target nucleic acids" or "target sequences". The term "target sequence" or "target nucleic acid" or grammatical equivalents herein

10 means a nucleic acid sequence on a single strand of nucleic acid. The target sequence may be a portion of a gene, a regulatory sequence, genomic DNA, cDNA, RNA including mRNA and rRNA, or others. As is outlined herein, the target sequence may be a target sequence from a sample, or a derivative target such as a product of a reaction such as a detection sequence from an Invader™ reaction, a ligated probe from an OLA reaction, an extended probe from an SBE reaction, etc. It may

15 be any length, with the understanding that longer sequences are more specific. As will be appreciated by those in the art, the complementary target sequence may take many forms. For example, it may be contained within a larger nucleic acid sequence, i.e. all or part of a gene or mRNA, a restriction fragment of a plasmid or genomic DNA, among others. As is outlined more fully below, probes are made to hybridize to target sequences to determine the presence or absence of the target sequence in

20 a sample. Generally speaking, this term will be understood by those skilled in the art. The target sequence may also be comprised of different target domains; for example, a first target domain of the sample target sequence may hybridize to a capture probe, a second target domain may hybridize to a portion of a label probe, etc. The target domains may be adjacent or separated as indicated. Unless specified, the terms "first" and "second" are not meant to confer an orientation of the sequences with

25 respect to the 5'-3' orientation of the target sequence. For example, assuming a 5'-3' orientation of the complementary target sequence, the first target domain may be located either 5' to the second domain, or 3' to the second domain. In addition, as will be appreciated by those in the art, the probes on the surface of the array (e.g. attached to the microspheres) may be attached in either orientation, either such that they have a free 3' end or a free 5' end.

As is more fully outlined below, the target sequence may comprise a position for which sequence information is desired, generally referred to herein as the "detection position" or "detection locus". In a preferred embodiment, the detection position is a single nucleotide, although in some embodiments, it may comprise a plurality of nucleotides, either contiguous with each other or separated by one or more

35 nucleotides. By "plurality" as used herein is meant at least two. As used herein, the base which basepairs with a detection position base in a hybrid is termed a "readout position" or an "interrogation position".

In some embodiments, as is outlined herein, the target sequence may not be the sample target

sequence but instead is a product of a reaction herein, sometimes referred to herein as a "secondary" or "derivative" target sequence. Thus, for example, in SBE, the extended primer may serve as the target sequence; similarly, in invasive cleavage variations, the cleaved detection sequence may serve as the target sequence.

If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification as needed, as will be appreciated by those in the art.

Once prepared, the target sequence can be used in a variety of reactions for a variety of reasons. For example, in a preferred embodiment, genotyping reactions are done. Similarly, these reactions can also be used to detect the presence or absence of a target sequence. Sequencing or amplification reactions are also preferred. In addition, in any reaction, quantitation of the amount of a target sequence may be done.

Furthermore, as outlined below for each reaction, many of these techniques may be used in a solution based assay, wherein the reaction is done in solution and a reaction product is bound to the array for subsequent detection, or in solid phase assays, where the reaction occurs on the surface and is detected.

In general, the present invention provides pairs of capture probes (nucleic acids that are attached to addresses on arrays) and adapter sequences (sequences that are either perfectly or substantially complementary to the capture probe sequences) that can be used in a wide variety of ways, to immobilize target nucleic acids (either primary targets, such as genomic DNA, mRNA or cDNA, or secondary targets such as amplicons from a nucleic acid amplification or extension reaction, as outlined herein) to the addresses of the array. Thus, all the sequences in the Tables include their complements, and either sequence can be used as a capture probe (e.g. spotted onto a surface or attached to a microsphere of an array) or as the adapter sequence that binds to the capture probe.

Accordingly, by "adapter sequences" or "adapters" or grammatical equivalents is meant a nucleic acid segment generally non-native or exogenous to a target molecule that is used to immobilize the target molecule to a solid support via binding to a capture probe sequence. In a preferred embodiment the adapter sequences and capture probes are selected from the sequences set forth in Table I, Table II, Table III or Table IV.

Table I includes the sequence of the preferred 4000 sequences labeled "Decoder (5'-3')", and inherent in this table are the complementary sequences as well. In addition, the invention includes oligonucleotides that are complementary to those depicted in Table 1.

Table II includes the sequence of the preferred adapter/capture probe sequences and their complementary sequence. Table 2 depicts a preferred subset of 3172 decoder oligonucleotides and their complementary probe oligonucleotides. Accordingly, the invention provides compositions comprising a sequence as outlined in Table 2. In addition, the invention provides a composition comprising a complementary binding pair as outlined in Table 2.

Table 3 includes a preferred subset of 768 decoder oligonucleotides and complementary probe sequences. In some embodiments it may be desirable to include a uniform base at a terminus of the oligonucleotide, such as a T at the 5' end as depicted in Table 4. The inclusion of this uniform or constant base facilitates uniform labeling of the oligonucleotides.

These sequences are used as decoder probes, capture probes or adapter sequences as outlined in U.S.S.N. 09/344,526 and PCT/US99/14387, and U.S.S.N.s 60/160,917 and 09/5656,463 all of which are expressly incorporated by reference in their entirety.

As will be appreciated by those in the art, the length of the capture probe/adapter sequences will vary, depending on the desired "strength" of binding and the number of different adapters desired. In a preferred embodiment, adapter sequences range from about 5 to about 500 basepairs in length, with from about 8 to about 100 being preferred, and from about 10 to about 50 being particularly preferred.

As will be appreciated by those in the art, it is desirable to have adapter sequences that do not have significant homology to naturally occurring target sequences, to avoid non-specific or erroneous binding of target sequences to the capture probes. Accordingly, preferred embodiments utilize some method to select useful adapter sequences. In a preferred embodiment the method is outlined in Figure 1. Briefly, random 24-mer (or could be any desired length as outlined herein), sequences were assembled and subjected to certain defined screening procedures including such steps as requiring that the T<sub>m</sub> of each of the sequence be within a pre-defined range. In addition the GC content must be balanced with the AT content and the self-complementarity must be minimized. In addition GC runs should be minimized, that is, runs of Gs or Cs should be reduced. In addition, decoder (adapter) to decoder (adapter) complementarity should be reduced so that the adapters do not hybridize with each other. Finally, the sequences are screened against a specified genomic database. In a preferred embodiment the adapters comprise at least one sequence selected from the sequences in Table I, Table II, Table III or Table IV.

In a preferred embodiment, the adapter sequences are chosen on the basis of a decoding step. As is more fully outlined below, a decoding step is used to decode random bead arrays. In this embodiment, a set of candidate capture probes is chosen; this may be done in a variety of ways. In a preferred embodiment, the sequences are generated randomly, each of a sufficient length to ensure a

low probability of occurring naturally. In some embodiments, for example when the array will be used with a particular organism's genome (e.g. the human genome, the *Drosophila* genome, etc. ), the sequences are compared to the genome as a first filter, for example to remove sequences that would cross hybridize. Additionally, further filtering may be done using well-known methods, such as known methods for selecting good PCR primers. These techniques generally include steps that remove sequences that may have a propensity to form secondary structures or otherwise to cross-hybridize. Additionally, sequences that have extremes of melting temperatures can be optionally discarded, depending on the planned assay conditions.

Once a set of candidate capture probes is obtained, an array comprising the capture probes is made, and a matching set of decoding probes comprising the adapter sequences (e.g. the complements of the capture probes), as more fully outlined below, is made. Decoding then proceeds. Probes that do not hybridize well, for whatever reason, will not decode well, generally due to weak signals, and are generally discarded. Probes that cross-hybridize will also not decode well, as they will give ambiguous or mixed decoding signals. Only probes that hybridize sufficiently strongly and specifically will decode. Thus, by setting suitable thresholds for signal strength and signal purity, adapter sequences that perform according to specified criteria are identified. Additionally, by setting a range on signal strength, capture probe/adapter sequence pairs that perform similarly (but hybridize specifically) are identified. In a preferred embodiment, decoding reactions are repeated, under a variety of conditions, to test the robustness of the sequence pair.

Once identified, the adapter sequences are added to target sequences in a variety of ways, as will be appreciated by those in the art. In a preferred embodiment, nucleic acid amplification reactions are done, as is generally outlined in "Detection of Nucleic Acid Amplification Reactions Using Bead Arrays" and "Sequence Determination of Nucleic Acids using Arrays with Microspheres", both of which were filed on October 22, 1999, (U.S.S.N.'s 60/161,148 and 09/425,633, respectively), both of which are hereby incorporated by reference in their entirety. These may be either target amplification or signal amplification. In general, the techniques can be described as follows. Most amplification techniques require one or more primers hybridizing to all or part the target sequence (e.g. that hybridize to a target domain). The adapter sequences can be added to one or more of the primers (depending on the configuration/orientation of the system and need) and the amplification reactions are run. Thus, for example, PCR primers comprising at least one adapter sequence (and preferably one on each PCR primer) may be used; one or both of the ligation probes of an OLA or LCR reaction may comprise an adapter sequence; the sequencing primers for pyrosequencing, single-base extension, reversible chain termination, etc., reactions may comprise an adapter sequence; either the invader probe or the signalling probe of invasive cleavage reactions can comprise an adapter sequence; etc. Similarly, for signal detection techniques, the probes may comprise adapter sequences, with preferred methods utilizing removal of the unreacted probes. In addition, primers may include universal priming sequences. That is, the adapters may additionally contain universal priming sequences for universal

amplification of products of any of the reactions described herein. Universal priming sequences are further outlined in 09/779376, filed February 7, 2001; 09/779202, filed February 7, 2001; 09/915231, filed July 24, 2001; 60/180810, filed February 7, 2000; and 60/297609, filed June 11, 2001; and 60/311194 filed August 9, 2001, all of which are expressly incorporated herein by reference.

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In an alternative embodiment, non-nucleic acid reactions are used to add adapter sequences to the nucleic acid targets. For example, for the direct detection of non-amplified target sequences (e.g. genomic DNA samples, etc.) on universal arrays, non-amplification methods are required. In this embodiment, binding partner pairs or chemical methods may be used. For example, one member of a binding partner pair may be attached to the adapter sequence and the other member attached to the target sequence. For example, the binding partner be a hapten or antigen, which will bind its binding partner. For example, suitable binding partner pairs include, but are not limited to: antigens (such as proteins (including peptides)) and antibodies (including fragments thereof (Fabs, etc.)); proteins and small molecules, including biotin/streptavidin and digoxigenin and antibodies; enzymes and substrates or inhibitors; other protein-protein interacting pairs; receptor-ligands; and carbohydrates and their binding partners, are also suitable binding pairs. Nucleic acid - nucleic acid binding proteins pairs are also useful. In general, the smaller of the pair is attached to the NTP (or the probe) for incorporation into the extension primer. Preferred binding partner pairs include, but are not limited to, biotin (or imino-biotin) and streptavidin, digoxigenin and Abs, and Prolinx™ reagents.

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In a preferred embodiment, chemical attachment methods are used. In this embodiment, chemical functional groups on each of the target sequences and adapter sequences are used. As is known in the art, this may be accomplished in a variety of ways. Preferred functional groups for attachment are amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the two sequences are joined together; for example, amino groups on each nucleic acid may be attached, for example using linkers as are known in the art; for example, homo- or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference).

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In a preferred embodiment, aptamers are used in the system. Aptamers are nucleic acids that can be made to bind to virtually any target analyte; see Bock et al., Nature 355:564 (1992); Femulok et al., Current Op. Chem. Biol. 2:230 (1998); and U.S. Patents 5,270,163, 5,475,096, 5,567,588, 5,595,877, 5,637,459, 5,683,867, 5,705,337, and related patents, hereby incorporated by reference.

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In a preferred embodiment, an array comprising capture probes that hybridize to adapter sequences is made, as outlined herein. In one embodiment aptamers, comprising adapter sequences, can be added. As will be appreciated by those in the art, the aptamers may be preassociated with their binding partners, e.g. target analytes, prior to introduction to the array, or not. In addition, the association between the adapter sequences on the aptamers and the capture probes can be made

covalent, for example through the use of reactive groups (e.g. psoralen) and appropriate activation.

In addition, the present invention is directed to the use of adapter sequences to assemble arrays comprising other target analytes.

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The adapter sequences may be chosen as outlined above. Preferably the adapters are selected from the sequences set forth in Table I, Table II, Table III or Table IV. These adapter sequences can then be added to the target analytes using a variety of techniques. In general, as described above, non-covalent attachment using binding partner pairs may be done, or covalent attachment using chemical moieties (including linkers).

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Advantages of using adapters include but are not limited to, for example, the ability to create universal arrays. That is, a single array is utilized with each capture probe designed to hybridize with a specific adapter. The adapters are joined to any number of target analytes, such as nucleic acids, as is described herein. Thus, the same array is used for vastly different target analytes. Furthermore, hybridization of adapters with capture probes results in non-covalent attachment of the target nucleic acid to the address of the array (e.g. a microsphere in some embodiments). As such, the target nucleic/adapter hybrid is easily removed, and the microsphere/capture probe can be re-used. In addition, the construction of kits is greatly facilitated by the use of adapters. For example, arrays or microspheres can be prepared that comprise the capture probe; the adapters can be packaged along with the microspheres for attachment to any target analyte of interest. Thus, one need only attach the adapter to the target analyte and disperse on the array for the construction of an array of target analytes.

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Accordingly the present invention provides kits comprising adapters. Preferably the kits include at least 1 nucleic acid sequence as set forth in Table 1. More preferably the kits include at least 10-25 nucleic acids, with at least 50 nucleic acids more preferred. Even more preferable are kits that include at least 100 nucleic acids with more than 1000 even more preferred and more than 2000 even more preferred.

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It should also be noted that the sequences defined herein can also be used in "sandwich" assay formats, wherein a capture extender probe comprising a first domain that will hybridize to the capture probe and a second domain that has a target specific domain is used. The capture extender probe hybridizes both to the target sequence and the capture probe, thereby immobilizing the target sequence on the array.

Once the adapter sequences are associated with the target analyte, including target nucleic acids, the compositions are added to an array comprising addresses comprising capture probes. In one embodiment a plurality of hybrid adapter sequence/target analytes are pooled prior to addition to an

array. All of the methods and compositions herein are drawn to compositions and methods for detecting the presence of target analytes, particularly nucleic acids, using adapter arrays.

Accordingly, the present invention provides array compositions comprising at least a first substrate with a surface comprising individual sites. The present system finds particular utility in array formats, i.e. wherein there is a matrix of capture probes (herein generally referred to "pads", "addresses" or "micro-locations"). By "array" or "biochip" herein is meant a plurality of nucleic acids in an array format; the size of the array will depend on the composition and end use of the array. Nucleic acids arrays are known in the art, and can be classified in a number of ways; both ordered arrays (e.g. the ability to resolve chemistries at discrete sites), and random arrays are included. Ordered arrays include, but are not limited to, those made using photolithography techniques (Affymetrix GeneChip™), spotting techniques (Synteni and others), printing techniques (Hewlett Packard and Rosetta), three dimensional "gel pad" arrays, etc. In one embodiment the ordered arrays include arrays that contain nucleic acids at known locations. That is, the adapters or capture probes described herein are immobilized at known locations on a substrate. By "known" locations is meant a site that is known or has been known.

In addition, adapters find use "liquid arrays". By "liquid arrays" is meant an array in solution for analysis, for example, by flow cytometry.

A preferred embodiment utilizes microspheres on a variety of substrates including fiber optic bundles, as are outlined in PCTs US98/21193, PCT US99/14387 and PCT US98/05025; WO98/50782; and U.S.S.N.s 09/287,573, 09/151,877, 09/256,943, 09/316,154, 60/119,323, 09/315,584; all of which are expressly incorporated by reference. While much of the discussion below is directed to the use of microsphere arrays on fiber optic bundles, any array format of nucleic acids on solid supports may be utilized.

Arrays containing from about 2 different bioactive agents (e.g. different beads, when beads are used) to many millions can be made, with very large arrays being possible. Generally, the array will comprise from two to as many as a billion or more, depending on the size of the beads and the substrate, as well as the end use of the array, thus very high density, high density, moderate density, low density and very low density arrays may be made. Preferred ranges for very high density arrays are from about 10,000,000 to about 2,000,000,000, with from about 100,000,000 to about 1,000,000,000 being preferred (all numbers being in square cm). High density arrays range about 100,000 to about 10,000,000, with from about 1,000,000 to about 5,000,000 being particularly preferred. Moderate density arrays range from about 10,000 to about 100,000 being particularly preferred, and from about 20,000 to about 50,000 being especially preferred. Low density arrays are generally less than 10,000, with from about 1,000 to about 5,000 being preferred. Very low density arrays are less than 1,000, with from about 10 to about 1000 being preferred, and from about 100 to about 500 being particularly preferred. In some embodiments, the compositions of the invention may

not be in array format; that is, for some embodiments, compositions comprising a single bioactive agent may be made as well. In addition, in some arrays, multiple substrates may be used, either of different or identical compositions. Thus for example, large arrays may comprise a plurality of smaller substrates.

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In addition, one advantage of the present compositions is that particularly through the use of fiber optic technology, extremely high density arrays can be made. Thus for example, because beads of 200  $\mu\text{m}$  or less (with beads of 200 nm possible) can be used, and very small fibers are known, it is possible to have as many as 40,000 or more (in some instances, 1 million) different elements (e.g. fibers and beads) in a 1  $\text{mm}^2$  fiber optic bundle, with densities of greater than 25,000,000 individual beads and fibers (again, in some instances as many as 50-100 million) per 0.5  $\text{cm}^2$  obtainable (4 million per square cm for 5  $\mu$  center-to-center and 100 million per square cm for 1  $\mu$  center-to-center).

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By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of beads and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates is very large. Possible substrates include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, optical fiber bundles; and a variety of other polymers. In general, the substrates allow optical detection and do not themselves appreciably fluoresce.

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Generally the substrate is flat (planar), although as will be appreciated by those in the art, other configurations of substrates may be used as well; for example, three dimensional configurations can be used, for example by embedding the beads in a porous block of plastic that allows sample access to the beads and using a confocal microscope for detection. Similarly, the beads may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Preferred substrates include optical fiber bundles as discussed below, and flat planar substrates such as glass, polystyrene and other plastics and acrylics.

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In a preferred embodiment, the substrate is an optical fiber bundle or array, as is generally described in U.S.S.N.s 08/944,850 and 08/519,062, PCT US98/05025, and PCT US98/09163, all of which are expressly incorporated herein by reference. Preferred embodiments utilize preformed unitary fiber optic arrays. By "preformed unitary fiber optic array" herein is meant an array of discrete individual fiber optic strands that are co-axially disposed and joined along their lengths. The fiber strands are generally individually clad. However, one thing that distinguished a preformed unitary array from other fiber optic formats is that the fibers are not individually physically manipulatable; that is, one strand



generally cannot be physically separated at any point along its length from another fiber strand.

At least one surface of the substrate is modified to contain discrete, individual sites for later association of microspheres. These sites may comprise physically altered sites, i.e. physical configurations such as wells or small depressions in the substrate that can retain the beads, such that a microsphere can rest in the well, or the use of other forces (magnetic or compressive), or chemically altered or active sites, such as chemically functionalized sites, electrostatically altered sites, hydrophobically/ hydrophilically functionalized sites, spots of adhesive, etc.

The sites may be a pattern, i.e. a regular design or configuration, or randomly distributed. A preferred embodiment utilizes a regular pattern of sites such that the sites may be addressed in the X-Y coordinate plane. "Pattern" in this sense includes a repeating unit cell, preferably one that allows a high density of beads on the substrate. However, it should be noted that these sites may not be discrete sites. That is, it is possible to use a uniform surface of adhesive or chemical functionalities, for example, that allows the attachment of beads at any position. That is, the surface of the substrate is modified to allow attachment of the microspheres at individual sites, whether or not those sites are contiguous or non-contiguous with other sites. Thus, the surface of the substrate may be modified such that discrete sites are formed that can only have a single associated bead, or alternatively, the surface of the substrate is modified and beads may go down anywhere, but they end up at discrete sites.

In a preferred embodiment, the surface of the substrate is modified to contain wells, i.e. depressions in the surface of the substrate. This may be done as is generally known in the art using a variety of techniques, including, but not limited to, photolithography, stamping techniques, molding techniques and microetching techniques. As will be appreciated by those in the art, the technique used will depend on the composition and shape of the substrate.

In a preferred embodiment, physical alterations are made in a surface of the substrate to produce the sites. In a preferred embodiment, the substrate is a fiber optic bundle and the surface of the substrate is a terminal end of the fiber bundle, as is generally described in 08/818,199 and 09/151,877, both of which are hereby expressly incorporated by reference. In this embodiment, wells are made in a terminal or distal end of a fiber optic bundle comprising individual fibers. In this embodiment, the cores of the individual fibers are etched, with respect to the cladding, such that small wells or depressions are formed at one end of the fibers. The required depth of the wells will depend on the size of the beads to be added to the wells.

Generally in this embodiment, the microspheres are non-covalently associated in the wells, although the wells may additionally be chemically functionalized as is generally described below, cross-linking agents may be used, or a physical barrier may be used, i.e. a film or membrane over the beads.

In a preferred embodiment, the surface of the substrate is modified to contain chemically modified sites, that can be used to attach, either covalently or non-covalently, the microspheres of the invention to the discrete sites or locations on the substrate. "Chemically modified sites" in this context includes, but is not limited to, the addition of a pattern of chemical functional groups including amino groups, carboxy groups, oxo groups and thiol groups, that can be used to covalently attach microspheres, which generally also contain corresponding reactive functional groups; the addition of a pattern of adhesive that can be used to bind the microspheres (either by prior chemical functionalization for the addition of the adhesive or direct addition of the adhesive); the addition of a pattern of charged groups (similar to the chemical functionalities) for the electrostatic attachment of the microspheres, i.e. when the microspheres comprise charged groups opposite to the sites; the addition of a pattern of chemical functional groups that renders the sites differentially hydrophobic or hydrophilic, such that the addition of similarly hydrophobic or hydrophilic microspheres under suitable experimental conditions will result in association of the microspheres to the sites on the basis of hydroaffinity. For example, the use of hydrophobic sites with hydrophobic beads, in an aqueous system, drives the association of the beads preferentially onto the sites. As outlined above, "pattern" in this sense includes the use of a uniform treatment of the surface to allow attachment of the beads at discrete sites, as well as treatment of the surface resulting in discrete sites. As will be appreciated by those in the art, this may be accomplished in a variety of ways.

In a preferred embodiment, the compositions of the invention further comprise a population of microspheres. By "population" herein is meant a plurality of beads as outlined above for arrays. Within the population are separate subpopulations, which can be a single microsphere or multiple identical microspheres. That is, in some embodiments, as is more fully outlined below, the array may contain only a single bead for each capture probe; preferred embodiments utilize a plurality of beads of each type.

By "microspheres" or "beads" or "particles" or grammatical equivalents herein is meant small discrete particles. The composition of the beads will vary, depending on the class of capture probe and the method of synthesis. Suitable bead compositions include those used in peptide, nucleic acid and organic moiety synthesis, including, but not limited to, plastics, ceramics, glass, polystyrene, methylstyrene, acrylic polymers, paramagnetic materials, thoria sol, carbon graphite, titanium dioxide, latex or cross-linked dextrans such as Sepharose, cellulose, nylon, cross-linked micelles and Teflon may all be used. *"Microsphere Detection Guide"* from Bangs Laboratories, Fishers IN is a helpful guide.

The beads need not be spherical; irregular particles may be used. In addition, the beads may be porous, thus increasing the surface area of the bead available for either capture probe attachment or tag attachment. The bead sizes range from nanometers, i.e. 100 nm, to millimeters, i.e. 1 mm, with beads from about 0.2 micron to about 200 microns being preferred, and from about 0.5 to about 5

micron being particularly preferred, although in some embodiments smaller beads may be used.

It should be noted that a key component of this embodiment of the invention is the use of a substrate/bead pairing that allows the association or attachment of the beads at discrete sites on the surface of the substrate, such that the beads do not move during the course of the assay.

Each microsphere comprises a capture probe, although as will be appreciated by those in the art, there may be some microspheres which do not contain a capture probe, depending on the synthetic methods. Alternatively, some have more than one capture probe.

Attachment of the nucleic acids may be done in a variety of ways, as will be appreciated by those in the art, including, but not limited to, chemical or affinity capture (for example, including the incorporation of derivatized nucleotides such as AminoLink or biotinylated nucleotides that can then be used to attach the nucleic acid to a surface, as well as affinity capture by hybridization), cross-linking, and electrostatic attachment, etc. In a preferred embodiment, affinity capture is used to attach the nucleic acids to the beads. For example, nucleic acids can be derivatized, for example with one member of a binding pair, and the beads derivatized with the other member of a binding pair. Suitable binding pairs are as described herein for IBL/DBL pairs. For example, the nucleic acids may be biotinylated (for example using enzymatic incorporation of biotinylated nucleotides, for by photoactivated cross-linking of biotin). Biotinylated nucleic acids can then be captured on streptavidin-coated beads, as is known in the art. Similarly, other hapten-receptor combinations can be used, such as digoxigenin and anti-digoxigenin antibodies. Alternatively, chemical groups can be added in the form of derivatized nucleotides, that can then be used to add the nucleic acid to the surface.

Preferred attachments are covalent, although even relatively weak interactions (i.e. non-covalent) can be sufficient to attach a nucleic acid to a surface, if there are multiple sites of attachment per each nucleic acid. Thus, for example, electrostatic interactions can be used for attachment, for example by having beads carrying the opposite charge to the bioactive agent.

Similarly, affinity capture utilizing hybridization can be used to attach nucleic acids to beads. For example, as is known in the art, polyA+RNA is routinely captured by hybridization to oligo-dT beads; this may include oligo-dT capture followed by a cross-linking step, such as psoralen crosslinking). If the nucleic acids of interest do not contain a polyA tract, one can be attached by polymerization with terminal transferase, or via ligation of an oligoA linker, as is known in the art.

Alternatively, chemical crosslinking may be done, for example by photoactivated crosslinking of thymidine to reactive groups, as is known in the art.

In a preferred embodiment, each bead comprises a single type of capture probe, although a plurality of

individual capture probes are preferably attached to each bead. Similarly, preferred embodiments utilize more than one microsphere containing a unique capture probe; that is, there is redundancy built into the system by the use of subpopulations of microspheres, each microsphere in the subpopulation containing the same capture probe.

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In an alternative embodiment, each bead comprises a plurality of different capture probes.

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As will be appreciated by those in the art, the capture probes may either be synthesized directly on the beads, or they may be made and then attached after synthesis. In a preferred embodiment, linkers are used to attach the capture probes to the beads, to allow both good attachment, sufficient flexibility to allow good interaction with the target molecule, and to avoid undesirable binding reactions.

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In a preferred embodiment, the capture probes are synthesized directly on the beads. As is known in the art, many classes of chemical compounds are currently synthesized on solid supports, such as peptides, organic moieties, and nucleic acids. It is a relatively straightforward matter to adjust the current synthetic techniques to use beads.

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In a preferred embodiment, the capture probes are synthesized first, and then covalently attached to the beads. As will be appreciated by those in the art, this will be done depending on the composition of the capture probes and the beads. The functionalization of solid support surfaces such as certain polymers with chemically reactive groups such as thiols, amines, carboxyls, etc. is generally known in the art. Accordingly, "blank" microspheres may be used that have surface chemistries that facilitate the attachment of the desired functionality by the user. Some examples of these surface chemistries for blank microspheres include, but are not limited to, amino groups including aliphatic and aromatic amines, carboxylic acids, aldehydes, amides, chloromethyl groups, hydrazide, hydroxyl groups, sulfonates and sulfates.

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In a preferred embodiment the attachment of nucleic acids to substrates includes contacting the oligonucleotide and the solid support in the presence of high salt concentrations. As is appreciated by those skilled in the art, salt includes, but is not limited to sodium chloride, potassium chloride, calcium chloride, magnesium chloride, lithium chloride, rubidium chloride, cesium chloride, barium chloride and the like. In a preferred embodiment, salt as used in the invention includes sodium chloride.

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By high salt concentrations is meant salt that is more concentrated than about 0.1 M salt. In a preferred embodiment, by high salt concentrations is meant greater than about 0.2 M salt. In a particularly preferred embodiment, high salt concentrations include from about 0.5 to 3M salt, with about 1M to 2M being most preferred.

By solid support or other grammatical equivalents herein is meant any material that can be modified

to contain oligonucleotides. As will be appreciated by those in the art, the number of possible solid supports is very large. Possible solid supports include, but are not limited to beads, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, optical fiber bundles, and a variety of other polymers.

Once formed, the support containing the oligonucleotides finds use in a variety of systems including decoding arrays as described in more detail in U.S.S.N. 09/344,526, and U.S.S.N. 09/574, 117, both of which are expressly incorporated herein by reference. In addition, the support containing the oligonucleotides finds use in microfluidic systems as described in U.S.S.N. 09/306,369 which is expressly incorporated herein by reference. In addition, the support containing the oligonucleotides finds use in composite array systems as described in U.S.S.N. 09/606,369, which is expressly incorporated herein by reference. In addition the support containing the oligonucleotides finds use in a variety of assays as outlined in more detail in U.S.S.N.s 09/513,362, 09/517,945, 09/535,854, 60/160,917, 60/180,810, 60/182,955, and 09/566,463, all of which are expressly incorporated herein by reference in their entirety. In addition, the support containing the oligonucleotides finds use in array based sensors as described in more detail in 09/287,573, 09/260,963, 09/450,829, 09/151,877, 09/187,289 and 08/519,062, all of which are expressly incorporated herein by reference in their entirety.

Accordingly the invention provides a method of attaching oligonucleotides to a solid support. The method includes contacting the oligonucleotides with the support in the presence of high salt as described herein. Once attached, as discussed in the examples, the attached oligonucleotides readily hybridize to targets, probes and the like. Attachment of crude oligonucleotides in the presence of high salt is as efficient as attaching purified oligonucleotides. Thus, the invention also contemplates a method of attachment of oligonucleotides to a solid support without prior purification of the oligonucleotides. Again, the method includes contacting the crude oligonucleotides with a solid support in the presence of high salt as described herein.

The capture probes are designed to be substantially complementary to the adapter sequences, to allow for a minimum of cross reactivity.

When microsphere arrays are used, an encoding/decoding system must be used. That is, since the beads are generally put onto the substrate randomly, there are several ways to correlate the functionality on the bead with its location, including the incorporation of unique optical signatures, generally fluorescent dyes, that could be used to identify the chemical functionality on any particular bead. This allows the synthesis of the candidate agents (i.e. compounds such as nucleic acids and

antibodies) to be divorced from their placement on an array, i.e. the candidate agents may be synthesized on the beads, and then the beads are randomly distributed on a patterned surface. Since the beads are first coded with an optical signature, this means that the array can later be "decoded", i.e. after the array is made, a correlation of the location of an individual site on the array with the bead or candidate agent at that particular site can be made. This means that the beads may be randomly distributed on the array, a fast and inexpensive process as compared to either the in situ synthesis or spotting techniques of the prior art.

However, the drawback to these methods is that for a large array, the system requires a large number of different optical signatures, which may be difficult or time-consuming to utilize. Accordingly, the present invention provides several improvements over these methods, generally directed to methods of coding and decoding the arrays. That is, as will be appreciated by those in the art, the placement of the capture probes is generally random, and thus a coding/decoding system is required to identify the probe at each location in the array. This may be done in a variety of ways, as is more fully outlined below, and generally includes: a) the use a decoding binding ligand (DBL), generally directly labeled, that binds to either the capture probe or to identifier binding ligands (IBLs) attached to the beads; b) positional decoding, for example by either targeting the placement of beads (for example by using photoactivatable or photocleavable moieties to allow the selective addition of beads to particular locations), or by using either sub-bundles or selective loading of the sites, as are more fully outlined below; c) selective decoding, wherein only those beads that bind to a target are decoded; or d) combinations of any of these. In some cases, as is more fully outlined below, this decoding may occur for all the beads, or only for those that bind a particular target sequence. Similarly, this may occur either prior to or after addition of a target sequence. In addition, as outlined herein, the target sequences detected may be either a primary target sequence (e.g. a patient sample), or a reaction product from one of the methods described herein (e.g. an extended SBE probe, a ligated probe, a cleaved signal probe, etc.).

Once the identity (i.e. the actual agent) and location of each microsphere in the array has been fixed, the array is exposed to samples containing the target sequences, although as outlined below, this can be done prior to or during the analysis as well. The target sequences can hybridize (either directly or indirectly) to the capture probes as is more fully outlined below, and results in a change in the optical signal of a particular bead.

In the present invention, "decoding" may not rely on the use of optical signatures, but rather on the use of decoding binding ligands that are added during a decoding step. The decoding binding ligands will bind either to a distinct identifier binding ligand partner that is placed on the beads, or to the capture probe itself. In this embodiment the decoding binding ligand either is complementary to the capture probe. In this embodiment the decoding binding ligand has the sequence of the adapter that also binds to the capture probe. In a preferred embodiment the decoder binding ligand is a nucleic acid

that has the sequence of at least one of the nucleic acids set forth in Table 1.

The decoding binding ligands are either directly or indirectly labeled, and thus decoding occurs by detecting the presence of the label. By using pools of decoding binding ligands in a sequential fashion, it is possible to greatly minimize the number of required decoding steps.

In some embodiments, the microspheres may additionally comprise identifier binding ligands for use in certain decoding systems. By "identifier binding ligands" or "IBLs" herein is meant a compound that will specifically bind a corresponding decoder binding ligand (DBL) to facilitate the elucidation of the identity of the capture probe attached to the bead. That is, the IBL and the corresponding DBL form a binding partner pair. By "specifically bind" herein is meant that the IBL binds its DBL with specificity sufficient to differentiate between the corresponding DBL and other DBLs (that is, DBLs for other IBLs), or other components or contaminants of the system. The binding should be sufficient to remain bound under the conditions of the decoding step, including wash steps to remove non-specific binding. In some embodiments, for example when the IBLs and corresponding DBLs are proteins or nucleic acids, the dissociation constants of the IBL to its DBL will be less than about  $10^{-4}$ - $10^{-8}$  M<sup>-1</sup>, with less than about  $10^{-5}$  to  $10^{-8}$  M<sup>-1</sup> being preferred and less than about  $10^{-7}$ - $10^{-8}$  M<sup>-1</sup> being particularly preferred.

IBL-DBL binding pairs are known or can be readily found using known techniques. For example, when the IBL is a protein, the DBLs include proteins (particularly including antibodies or fragments thereof (FABs, etc.)) or small molecules, or vice versa (the IBL is an antibody and the DBL is a protein). Metal ion-metal ion ligands or chelators pairs are also useful. Antigen-antibody pairs, enzymes and substrates or inhibitors, other protein-protein interacting pairs, receptor-ligands, complementary nucleic acids, and carbohydrates and their binding partners are also suitable binding pairs. Nucleic acid-nucleic acid binding proteins pairs are also useful. Similarly, as is generally described in U.S. Patents 5,270,163, 5,475,096, 5,567,588, 5,595,877, 5,637,459, 5,683,867, 5,705,337, and related patents, hereby incorporated by reference, nucleic acid "aptamers" can be developed for binding to virtually any target; such an aptamer-target pair can be used as the IBL-DBL pair. Similarly, there is a wide body of literature relating to the development of binding pairs based on combinatorial chemistry methods.

In a preferred embodiment, the IBL is a molecule whose color or luminescence properties change in the presence of a selectively-binding DBL. For example, the IBL may be a fluorescent pH indicator whose emission intensity changes with pH. Similarly, the IBL may be a fluorescent ion indicator, whose emission properties change with ion concentration.

Alternatively, the IBL is a molecule whose color or luminescence properties change in the presence of various solvents. For example, the IBL may be a fluorescent molecule such as an ethidium salt whose

fluorescence intensity increases in hydrophobic environments. Similarly, the IBL may be a derivative of fluorescein whose color changes between aqueous and nonpolar solvents.

5 In one embodiment, the DBL may be attached to a bead, i.e. a "decoder bead", that may carry a label such as a fluorophore.

10 In a preferred embodiment, the IBL-DBL pair comprise substantially complementary single-stranded nucleic acids. In this embodiment, the binding ligands can be referred to as "identifier probes" and "decoder probes". Generally, the identifier and decoder probes range from about 4 basepairs in length to about 1000, with from about 6 to about 100 being preferred, and from about 8 to about 40 being particularly preferred. What is important is that the probes are long enough to be specific, i.e. to distinguish between different IBL-DBL pairs, yet short enough to allow both a) dissociation, if necessary, under suitable experimental conditions, and b) efficient hybridization.

15 In a preferred embodiment, as is more fully outlined below, the IBLs do not bind to DBLs. Rather, the IBLs are used as identifier moieties ("IMs") that are identified directly, for example through the use of mass spectroscopy.

20 Alternatively, in a preferred embodiment, the IBL and the capture probe are the same moiety; thus, for example, as outlined herein, particularly when no optical signatures are used, the capture probe can serve as both the identifier and the agent. For example, in the case of nucleic acids, the bead-bound probe (which serves as the capture probe) can also bind decoder probes, to identify the sequence of the probe on the bead. Thus, in this embodiment, the DBLs bind to the capture probes.

25 In one embodiment, the microspheres may contain an optical signature. That is, as outlined in U.S.S.N.s 08/818,199 and 09/151,877, previous work had each subpopulation of microspheres comprising a unique optical signature or optical tag that is used to identify the unique capture probe of that subpopulation of microspheres; that is, decoding utilizes optical properties of the beads such that a bead comprising the unique optical signature may be distinguished from beads at other locations with different optical signatures. Thus the previous work assigned each capture probe a unique optical signature such that any microspheres comprising that capture probe are identifiable on the basis of the signature. These optical signatures comprised dyes, usually chromophores or fluorophores, that were entrapped or attached to the beads themselves. Diversity of optical signatures utilized different fluorochromes, different ratios of mixtures of fluorochromes, and different concentrations (intensities) of fluorochromes.

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In a preferred embodiment, the present invention does not rely solely on the use of optical properties to decode the arrays. However, as will be appreciated by those in the art, it is possible in some embodiments to utilize optical signatures as an additional coding method, in conjunction with the



present system. Thus, for example, as is more fully outlined below, the size of the array may be effectively increased while using a single set of decoding moieties in several ways, one of which is the use of optical signatures on some beads. Thus, for example, using one "set" of decoding molecules, the use of two populations of beads, one with an optical signature and one without, allows the effective doubling of the array size. The use of multiple optical signatures similarly increases the possible size of the array.

In a preferred embodiment, each subpopulation of beads comprises a plurality of different IBLs. By using a plurality of different IBLs to encode each capture probe, the number of possible unique codes is substantially increased. That is, by using one unique IBL per capture probe, the size of the array will be the number of unique IBLs (assuming no "reuse" occurs, as outlined below). However, by using a plurality of different IBLs per bead,  $n$ , the size of the array can be increased to  $2^n$ , when the presence or absence of each IBL is used as the indicator. For example, the assignment of 10 IBLs per bead generates a 10 bit binary code, where each bit can be designated as "1" (IBL is present) or "0" (IBL is absent). A 10 bit binary code has  $2^{10}$  possible variants. However, as is more fully discussed below, the size of the array may be further increased if another parameter is included such as concentration or intensity; thus for example, if two different concentrations of the IBL are used, then the array size increases as  $3^n$ . Thus, in this embodiment, each individual capture probe in the array is assigned a combination of IBLs, which can be added to the beads prior to the addition of the capture probe, after, or during the synthesis of the capture probe, i.e. simultaneous addition of IBLs and capture probe components.

Alternatively, the combination of different IBLs can be used to elucidate the sequence of the nucleic acid. Thus, for example, using two different IBLs (IBL1 and IBL2), the first position of a nucleic acid can be elucidated: for example, adenosine can be represented by the presence of both IBL1 and IBL2; thymidine can be represented by the presence of IBL1 but not IBL2, cytosine can be represented by the presence of IBL2 but not IBL1, and guanosine can be represented by the absence of both. The second position of the nucleic acid can be done in a similar manner using IBL3 and IBL4; thus, the presence of IBL1, IBL2, IBL3 and IBL4 gives a sequence of AA; IBL1, IBL2, and IBL3 shows the sequence AT; IBL1, IBL3 and IBL4 gives the sequence TA, etc. The third position utilizes IBL5 and IBL6, etc. In this way, the use of 20 different identifiers can yield a unique code for every possible 10-mer.

In this way, a sort of "bar code" for each sequence can be constructed; the presence or absence of each distinct IBL will allow the identification of each capture probe.

In addition, the use of different concentrations or densities of IBLs allows a "reuse" of sorts. If, for example, the bead comprising a first agent has a 1X concentration of IBL, and a second bead comprising a second agent has a 10X concentration of IBL, using saturating concentrations of the

corresponding labelled DBL allows the user to distinguish between the two beads.

Once the microspheres comprising the capture probes are generated, they are added to the substrate to form an array. It should be noted that while most of the methods described herein add the beads to the substrate prior to the assay, the order of making, using and decoding the array can vary. For example, the array can be made, decoded, and then the assay done. Alternatively, the array can be made, used in an assay, and then decoded; this may find particular use when only a few beads need be decoded. Alternatively, the beads can be added to the assay mixture, i.e. the sample containing the target sequences, prior to the addition of the beads to the substrate; after addition and assay, the array may be decoded. This is particularly preferred when the sample comprising the beads is agitated or mixed; this can increase the amount of target sequence bound to the beads per unit time, and thus (in the case of nucleic acid assays) increase the hybridization kinetics. This may find particular use in cases where the concentration of target sequence in the sample is low; generally, for low concentrations, long binding times must be used.

In general, the methods of making the arrays and of decoding the arrays is done to maximize the number of different candidate agents that can be uniquely encoded. The compositions of the invention may be made in a variety of ways. In general, the arrays are made by adding a solution or slurry comprising the beads to a surface containing the sites for attachment of the beads. This may be done in a variety of buffers, including aqueous and organic solvents, and mixtures. The solvent can evaporate, and excess beads are removed.

In a preferred embodiment, when non-covalent methods are used to associate the beads with the array, a novel method of loading the beads onto the array is used. This method comprises exposing the array to a solution of particles (including microspheres and cells) and then applying energy, e.g. agitating or vibrating the mixture. This results in an array comprising more tightly associated particles, as the agitation is done with sufficient energy to cause weakly-associated beads to fall off (or out, in the case of wells). These sites are then available to bind a different bead. In this way, beads that exhibit a high affinity for the sites are selected. Arrays made in this way have two main advantages as compared to a more static loading: first of all, a higher percentage of the sites can be filled easily, and secondly, the arrays thus loaded show a substantial decrease in bead loss during assays. Thus, in a preferred embodiment, these methods are used to generate arrays that have at least about 50% of the sites filled, with at least about 75% being preferred, and at least about 90% being particularly preferred. Similarly, arrays generated in this manner preferably lose less than about 20% of the beads during an assay, with less than about 10% being preferred and less than about 5% being particularly preferred.

In this embodiment, the substrate comprising the surface with the discrete sites is immersed into a solution comprising the particles (beads, cells, etc.). The surface may comprise wells, as is described

herein, or other types of sites on a patterned surface such that there is a differential affinity for the sites. This differential affinity results in a competitive process, such that particles that will associate more tightly are selected. Preferably, the entire surface to be "loaded" with beads is in fluid contact with the solution. This solution is generally a slurry ranging from about 10,000:1 beads:solution (vol:vol) to 1:1. Generally, the solution can comprise any number of reagents, including aqueous buffers, organic solvents, salts, other reagent components, etc. In addition, the solution preferably comprises an excess of beads; that is, there are more beads than sites on the array. Preferred embodiments utilize two-fold to billion-fold excess of beads.

The immersion can mimic the assay conditions; for example, if the array is to be "dipped" from above into a microtiter plate comprising samples, this configuration can be repeated for the loading, thus minimizing the beads that are likely to fall out due to gravity.

Once the surface has been immersed, the substrate, the solution, or both are subjected to a competitive process, whereby the particles with lower affinity can be disassociated from the substrate and replaced by particles exhibiting a higher affinity to the site. This competitive process is done by the introduction of energy, in the form of heat, sonication, stirring or mixing, vibrating or agitating the solution or substrate, or both.

A preferred embodiment utilizes agitation or vibration. In general, the amount of manipulation of the substrate is minimized to prevent damage to the array; thus, preferred embodiments utilize the agitation of the solution rather than the array, although either will work. As will be appreciated by those in the art, this agitation can take on any number of forms, with a preferred embodiment utilizing microtiter plates comprising bead solutions being agitated using microtiter plate shakers.

The agitation proceeds for a period of time sufficient to load the array to a desired fill. Depending on the size and concentration of the beads and the size of the array, this time may range from about 1 second to days, with from about 1 minute to about 24 hours being preferred.

It should be noted that not all sites of an array may comprise a bead; that is, there may be some sites on the substrate surface which are empty. In addition, there may be some sites that contain more than one bead, although this is not preferred.

In some embodiments, for example when chemical attachment is done, it is possible to attach the beads in a non-random or ordered way. For example, using photoactivatable attachment linkers or photoactivatable adhesives or masks, selected sites on the array may be sequentially rendered suitable for attachment, such that defined populations of beads are laid down.

The arrays of the present invention are constructed such that information about the identity of the

capture probe is built into the array, such that the random deposition of the beads in the fiber wells can be "decoded" to allow identification of the capture probe at all positions. This may be done in a variety of ways, and either before, during or after the use of the array to detect target molecules.

5 Thus, after the array is made, it is "decoded" in order to identify the location of one or more of the capture probes, i.e. each subpopulation of beads, on the substrate surface.

In a preferred embodiment, pyrosequencing techniques are used to decode the array, as is generally described in "Nucleic Acid Sequencing using Microsphere Arrays", filed October 22, 1999 (no U.S.S.N. received yet), hereby incorporated by reference.

10 In a preferred embodiment, a selective decoding system is used. In this case, only those microspheres exhibiting a change in the optical signal as a result of the binding of a target sequence are decoded. This is commonly done when the number of "hits", i.e. the number of sites to decode, is generally low. That is, the array is first scanned under experimental conditions in the absence of the target sequences. The sample containing the target sequences is added, and only those locations exhibiting a change in the optical signal are decoded. For example, the beads at either the positive or negative signal locations may be either selectively tagged or released from the array (for example through the use of photocleavable linkers), and subsequently sorted or enriched in a fluorescence-activated cell sorter (FACS). That is, either all the negative beads are released, and then the positive beads are either released or analyzed in situ, or alternatively all the positives are released and analyzed. Alternatively, the labels may comprise halogenated aromatic compounds, and detection of the label is done using for example gas chromatography, chemical tags, isotopic tags mass spectral tags.

25 As will be appreciated by those in the art, this may also be done in systems where the array is not decoded; i.e. there need not ever be a correlation of bead composition with location. In this embodiment, the beads are loaded on the array, and the assay is run. The "positives", i.e. those beads displaying a change in the optical signal as is more fully outlined below, are then "marked" to distinguish or separate them from the "negative" beads. This can be done in several ways, preferably using fiber optic arrays. In a preferred embodiment, each bead contains a fluorescent dye. After the assay and the identification of the "positives" or "active beads", light is shown down either only the positive fibers or only the negative fibers, generally in the presence of a light-activated reagent (typically dissolved oxygen). In the former case, all the active beads are photobleached. Thus, upon non-selective release of all the beads with subsequent sorting, for example using a fluorescence activated cell sorter (FACS) machine, the non-fluorescent active beads can be sorted from the fluorescent negative beads. Alternatively, when light is shown down the negative fibers, all the negatives are non-fluorescent and the positives are fluorescent, and sorting can proceed. The characterization of the attached capture probe may be done directly, for example using mass

spectroscopy.

Alternatively, the identification may occur through the use of identifier moieties ("IMs"), which are similar to IBLs but need not necessarily bind to DBLs. That is, rather than elucidate the structure of the capture probe directly, the composition of the IMs may serve as the identifier. Thus, for example, a specific combination of IMs can serve to code the bead, and be used to identify the agent on the bead upon release from the bead followed by subsequent analysis, for example using a gas chromatograph or mass spectroscope.

Alternatively, rather than having each bead contain a fluorescent dye, each bead comprises a non-fluorescent precursor to a fluorescent dye. For example, using photocleavable protecting groups, such as certain ortho-nitrobenzyl groups, on a fluorescent molecule, photoactivation of the fluorochrome can be done. After the assay, light is shown down again either the "positive" or the "negative" fibers, to distinguish these populations. The illuminated precursors are then chemically converted to a fluorescent dye. All the beads are then released from the array, with sorting, to form populations of fluorescent and non-fluorescent beads (either the positives and the negatives or vice versa).

In an alternate preferred embodiment, the sites of attachment of the beads (for example the wells) include a photopolymerizable reagent, or the photopolymerizable agent is added to the assembled array. After the test assay is run, light is shown down again either the "positive" or the "negative" fibers, to distinguish these populations. As a result of the irradiation, either all the positives or all the negatives are polymerized and trapped or bound to the sites, while the other population of beads can be released from the array.

In a preferred embodiment, the location of every capture probe is determined using decoder binding ligands (DBLs). As outlined above, DBLs are binding ligands that will either bind to identifier binding ligands, if present, or to the capture probes themselves, preferably when the capture probe is a nucleic acid or protein.

In a preferred embodiment, as outlined above, the DBL binds to the IBL.

In a preferred embodiment, the capture probes are single-stranded nucleic acids and the DBL is a substantially complementary single-stranded nucleic acid that binds (hybridizes) to the capture probe, termed a decoder probe herein. A decoder probe that is substantially complementary to each candidate probe is made and used to decode the array. In this embodiment, the candidate probes and the decoder probes should be of sufficient length (and the decoding step run under suitable conditions) to allow specificity; i.e. each candidate probe binds to its corresponding decoder probe with sufficient specificity to allow the distinction of each candidate probe.

In a preferred embodiment, the DBLs are either directly or indirectly labeled. In a preferred embodiment, the DBL is directly labeled, that is, the DBL comprises a label. In an alternate embodiment, the DBL is indirectly labeled; that is, a labeling binding ligand (LBL) that will bind to the DBL is used. In this embodiment, the labeling binding ligand-DBL pair can be as described above for IBL-DBL pairs.

Accordingly, the identification of the location of the individual beads (or subpopulations of beads) is done using one or more decoding steps comprising a binding between the labeled DBL and either the IBL or the capture probe (i.e. a hybridization between the candidate probe and the decoder probe when the capture probe is a nucleic acid). After decoding, the DBLs can be removed and the array can be used; however, in some circumstances, for example when the DBL binds to an IBL and not to the capture probe, the removal of the DBL is not required (although it may be desirable in some circumstances). In addition, as outlined herein, decoding may be done either before the array is used to in an assay, during the assay, or after the assay.

In one embodiment, a single decoding step is done. In this embodiment, each DBL is labeled with a unique label, such that the the number of unique tags is equal to or greater than the number of capture probes (although in some cases, "reuse" of the unique labels can be done, as described herein; similarly, minor variants of candidate probes can share the same decoder, if the variants are encoded in another dimension, i.e. in the bead size or label). For each capture probe or IBL, a DBL is made that will specifically bind to it and contains a unique tag, for example one or more fluorochromes. Thus, the identity of each DBL, both its composition (i.e. its sequence when it is a nucleic acid) and its label, is known. Then, by adding the DBLs to the array containing the capture probes under conditions which allow the formation of complexes (termed hybridization complexes when the components are nucleic acids) between the DBLs and either the capture probes or the IBLs, the location of each DBL can be elucidated. This allows the identification of the location of each capture probe; the random array has been decoded. The DBLs can then be removed, if necessary, and the target sample applied.

In a preferred embodiment, the number of unique labels is less than the number of unique capture probes, and thus a sequential series of decoding steps are used. In this embodiment, decoder probes are divided into  $n$  sets for decoding. The number of sets corresponds to the number of unique tags. Each decoder probe is labeled in  $n$  separate reactions with  $n$  distinct tags. All the decoder probes share the same  $n$  tags. The decoder probes are pooled so that each pool contains only one of the  $n$  tag versions of each decoder, and no two decoder probes have the same sequence of tags across all the pools. The number of pools required for this to be true is determined by the number of decoder probes and the  $n$ . Hybridization of each pool to the array generates a signal at every address. The sequential hybridization of each pool in turn will generate a unique, sequence-specific code for each candidate probe. This identifies the candidate probe at each address in the array. For example, if four

tags are used, then  $4 \times n$  sequential hybridizations can ideally distinguish  $4^n$  sequences, although in some cases more steps may be required. After the hybridization of each pool, the hybrids are denatured and the decoder probes removed, so that the probes are rendered single-stranded for the next hybridization (although it is also possible to hybridize limiting amounts of target so that the available probe is not saturated. Sequential hybridizations can be carried out and analyzed by subtracting pre-existing signal from the previous hybridization).

An example is illustrative. Assuming an array of 16 probe nucleic acids (numbers 1-16), and four unique tags (four different fluors, for example; labels A-D). Decoder probes 1-16 are made that correspond to the probes on the beads. The first step is to label decoder probes 1-4 with tag A, decoder probes 5-8 with tag B, decoder probes 9-12 with tag C, and decoder probes 13-16 with tag D. The probes are mixed and the pool is contacted with the array containing the beads with the attached candidate probes. The location of each tag (and thus each decoder and candidate probe pair) is then determined. The first set of decoder probes are then removed. A second set is added, but this time, decoder probes 1, 5, 9 and 13 are labeled with tag A, decoder probes 2, 6, 10 and 14 are labeled with tag B, decoder probes 3, 7, 11 and 15 are labeled with tag C, and decoder probes 4, 8, 12 and 16 are labeled with tag D. Thus, those beads that contained tag A in both decoding steps contain candidate probe 1; tag A in the first decoding step and tag B in the second decoding step contain candidate probe 2; tag A in the first decoding step and tag C in the second step contain candidate probe 3; etc. In one embodiment, the decoder probes are labeled in situ; that is, they need not be labeled prior to the decoding reaction. In this embodiment, the incoming decoder probe is shorter than the candidate probe, creating a 5' "overhang" on the decoding probe. The addition of labeled ddNTPs (each labeled with a unique tag) and a polymerase will allow the addition of the tags in a sequence specific manner, thus creating a sequence-specific pattern of signals. Similarly, other modifications can be done, including ligation, etc.

In addition, since the size of the array will be set by the number of unique decoding binding ligands, it is possible to "reuse" a set of unique DBLs to allow for a greater number of test sites. This may be done in several ways; for example, by using some subpopulations that comprise optical signatures. Similarly, the use of a positional coding scheme within an array; different sub-bundles may reuse the set of DBLs. Similarly, one embodiment utilizes bead size as a coding modality, thus allowing the reuse of the set of unique DBLs for each bead size. Alternatively, sequential partial loading of arrays with beads can also allow the reuse of DBLs. Furthermore, "code sharing" can occur as well.

In a preferred embodiment, the DBLs may be reused by having some subpopulations of beads comprise optical signatures. In a preferred embodiment, the optical signature is generally a mixture of reporter dyes, preferably fluorescent. By varying both the composition of the mixture (i.e. the ratio of one dye to another) and the concentration of the dye (leading to differences in signal intensity), matrices of unique optical signatures may be generated. This may be done by covalently attaching the

dyes to the surface of the beads, or alternatively, by entrapping the dye within the bead.

In a preferred embodiment, the encoding can be accomplished in a ratio of at least two dyes, although more encoding dimensions may be added in the size of the beads, for example. In addition, the labels are distinguishable from one another; thus two different labels may comprise different molecules (i.e. two different fluorors) or, alternatively, one label at two different concentrations or intensity.

In a preferred embodiment, the dyes are covalently attached to the surface of the beads. This may be done as is generally outlined for the attachment of the capture probes, using functional groups on the surface of the beads. As will be appreciated by those in the art, these attachments are done to minimize the effect on the dye.

In a preferred embodiment, the dyes are non-covalently associated with the beads, generally by entrapping the dyes in the pores of the beads.

Additionally, encoding in the ratios of the two or more dyes, rather than single dye concentrations, is preferred since it provides insensitivity to the intensity of light used to interrogate the reporter dye's signature and detector sensitivity.

In a preferred embodiment, a spatial or positional coding system is done. In this embodiment, there are sub-bundles or subarrays (i.e. portions of the total array) that are utilized. By analogy with the telephone system, each subarray is an "area code", that can have the same tags (i.e. telephone numbers) of other subarrays, that are separated by virtue of the location of the subarray. Thus, for example, the same unique tags can be reused from bundle to bundle. Thus, the use of 50 unique tags in combination with 100 different subarrays can form an array of 5000 different capture probes. In this embodiment, it becomes important to be able to identify one bundle from another; in general, this is done either manually or through the use of marker beads, i.e. beads containing unique tags for each subarray.

In alternative embodiments, additional encoding parameters can be added, such as microsphere size. For example; the use of different size beads may also allow the reuse of sets of DBLs; that is, it is possible to use microspheres of different sizes to expand the encoding dimensions of the microspheres. Optical fiber arrays can be fabricated containing pixels with different fiber diameters or cross-sections; alternatively, two or more fiber optic bundles, each with different cross-sections of the individual fibers, can be added together to form a larger bundle; or, fiber optic bundles with fiber of the same size cross-sections can be used, but just with different sized beads. With different diameters, the largest wells can be filled with the largest microspheres and then moving onto progressively smaller microspheres in the smaller wells until all size wells are then filled. In this manner, the same dye ratio could be used to encode microspheres of different sizes thereby expanding the number of



different oligonucleotide sequences or chemical functionalities present in the array. Although outlined for fiber optic substrates, this as well as the other methods outlined herein can be used with other substrates and with other attachment modalities as well.

5 In a preferred embodiment, the coding and decoding is accomplished by sequential loading of the microspheres into the array. As outlined above for spatial coding, in this embodiment, the optical signatures can be "reused". In this embodiment, the library of microspheres each comprising a different capture probe (or the subpopulations each comprise a different capture probe), is divided into a plurality of sublibraries; for example, depending on the size of the desired array and the number of  
10 unique tags, 10 sublibraries each comprising roughly 10% of the total library may be made, with each sublibrary comprising roughly the same unique tags. Then, the first sublibrary is added to the fiber optic bundle comprising the wells, and the location of each capture probe is determined, generally through the use of DBLs. The second sublibrary is then added, and the location of each capture probe is again determined. The signal in this case will comprise the signal from the "first" DBL and the  
15 "second" DBL; by comparing the two matrices the location of each bead in each sublibrary can be determined. Similarly, adding the third, fourth, etc. sublibraries sequentially will allow the array to be filled.

In a preferred embodiment, codes can be "shared" in several ways. In a first embodiment, a single  
20 code (i.e. IBL/DBL pair) can be assigned to two or more agents if the target sequences differ sufficiently in their binding strengths. For example, two nucleic acid probes used in an mRNA quantitation assay can share the same code if the ranges of their hybridization signal intensities do not overlap. This can occur, for example, when one of the target sequences is always present at a much higher concentration than the other. Alternatively, the two target sequences might always be present  
25 at a similar concentration, but differ in hybridization efficiency.

Alternatively, a single code can be assigned to multiple agents if the agents are functionally equivalent. For example, if a set of oligonucleotide probes are designed with the common purpose of detecting the presence of a particular gene, then the probes are functionally equivalent, even though they may  
30 differ in sequence. Similarly, an array of this type could be used to detect homologs of known genes. In this embodiment, each gene is represented by a heterologous set of probes, hybridizing to different regions of the gene (and therefore differing in sequence). The set of probes share a common code. If a homolog is present, it might hybridize to some but not all of the probes. The level of homology might be indicated by the fraction of probes hybridizing, as well as the average hybridization intensity.  
35 Similarly, multiple antibodies to the same protein could all share the same code.

In a preferred embodiment, decoding of self-assembled random arrays is done on the bases of pH titration. In this embodiment, in addition to capture probes, the beads comprise optical signatures, wherein the optical signatures are generated by the use of pH-responsive dyes (sometimes referred to

herein as "pH dyes") such as fluorophores. This embodiment is similar to that outlined in PCT US98/05025 and U.S.S.N. 09/151,877, both of which are expressly incorporated by reference, except that the dyes used in the present invention exhibit changes in fluorescence intensity (or other properties) when the solution pH is adjusted from below the pKa to above the pKa (or vice versa). In a preferred embodiment, a set of pH dyes are used, each with a different pKa, preferably separated by at least 0.5 pH units. Preferred embodiments utilize a pH dye set of pKa's of 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0, 9.5, 10.0, 10.5, 11, and 11.5. Each bead can contain any subset of the pH dyes, and in this way a unique code for the capture probe is generated. Thus, the decoding of an array is achieved by titrating the array from pH 1 to pH 13, and measuring the fluorescence signal from each bead as a function of solution pH.

Thus, the present invention provides array compositions comprising a substrate with a surface comprising discrete sites. A population of microspheres is distributed on the sites, and the population comprises at least a first and a second subpopulation. Each subpopulation comprises a capture probe, and, in addition, at least one optical dye with a given pKa. The pKas of the different optical dyes are different.

In a preferred embodiment, "random" decoding probes can be made. By sequential hybridizations or the use of multiple labels, as is outlined above, a unique hybridization pattern can be generated for each sensor element. This allows all the beads representing a given clone to be identified as belonging to the same group. In general, this is done by using random or partially degenerate decoding probes, that bind in a sequence-dependent but not highly sequence-specific manner. The process can be repeated a number of times, each time using a different labeling entity, to generate a different pattern of signals based on quasi-specific interactions. In this way, a unique optical signature is eventually built up for each sensor element. By applying pattern recognition or clustering algorithms to the optical signatures, the beads can be grouped into sets that share the same signature (i.e. carry the same probes).

In order to identify the actual sequence of the clone itself, additional procedures are required; for example, direct sequencing can be done, or an ordered array containing the clones, such as a spotted cDNA array, to generate a "key" that links a hybridization pattern to a specific clone.

Alternatively, clone arrays can be decoded using binary decoding with vector tags. For example, partially randomized oligos are cloned into a nucleic acid vector (e.g. plasmid, phage, etc.). Each oligonucleotide sequence consists of a subset of a limited set of sequences. For example, if the limited set comprises 10 sequences, each oligonucleotide may have some subset (or all of the 10) sequences. Thus each of the 10 sequences can be present or absent in the oligonucleotide. Therefore, there are  $2^{10}$  or 1,024 possible combinations. The sequences may overlap, and minor variants can also be represented (e.g. A, C, T and G substitutions) to increase the number of possible

combinations. A nucleic acid library is cloned into a vector containing the random code sequences. Alternatively, other methods such as PCR can be used to add the tags. In this way it is possible to use a small number of oligo decoding probes to decode an array of clones.

5 As will be appreciated by those in the art, the systems of the invention may take on a large number of different configurations, as is generally depicted in the Figures. In general, there are three types of systems that can be used: (1) "non-sandwich" systems (also referred to herein as "direct" detection) in which the target sequence itself is labeled with detectable labels (again, either because the primers  
10 comprise labels or due to the incorporation of labels into the newly synthesized strand); (2) systems in which label probes directly bind to the target analytes; and (3) systems in which label probes are indirectly bound to the target sequences, for example through the use of amplifier probes.

Detection of the reactions of the invention, including the direct detection of products and indirect detection utilizing label probes (i.e. sandwich assays), is preferably done by detecting assay  
15 complexes comprising detectable labels, which can be attached to the assay complex in a variety of ways.

In a preferred embodiment, an array of different and usually artificial capture probes are made; that is, the capture probes do not have complementarity to known target sequences. The adapter sequences  
20 can then be added to any target sequences, or soluble capture extender probes are made; this allows the manufacture of only one kind of array, with the user able to customize the array through the use of adapter sequences or capture extender probes. This then allows the generation of customized soluble probes, which as will be appreciated by those in the art is generally simpler and less costly.

25 When capture extender probes are used, in one embodiment, microsphere arrays containing a single type of capture probe are made; in this embodiment, the capture extender probes are added to the beads prior to loading on the array. The capture extender probes may be additionally fixed or crosslinked, as necessary.

30 Accordingly, the present invention provides compositions and methods for detecting the presence or absence of target analytes, including nucleic acid sequences, in a sample. As will be appreciated by those in the art, the sample solution may comprise any number of things, including, but not limited to, bodily fluids (including, but not limited to, blood, urine, serum, lymph, saliva, anal and vaginal secretions, perspiration and semen, of virtually any organism, with mammalian samples being  
35 preferred and human samples being particularly preferred); environmental samples (including, but not limited to, air, agricultural, water and soil samples); biological warfare agent samples; research samples (i.e. in the case of nucleic acids, the sample may be the products of an amplification reaction, including both target and signal amplification); purified samples, such as purified genomic DNA, RNA, proteins, etc.; raw samples (bacteria, virus, genomic DNA, etc.; As will be appreciated by those in the

art, virtually any experimental manipulation may have been done on the sample.

The present invention provides compositions and methods for detecting the presence or absence of target nucleic acid sequences in a sample.

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In a preferred embodiment, several levels of redundancy are built into the arrays of the invention. Building redundancy into an array gives several significant advantages, including the ability to make quantitative estimates of confidence about the data and significant increases in sensitivity. Thus, preferred embodiments utilize array redundancy. As will be appreciated by those in the art, there are at least two types of redundancy that can be built into an array: the use of multiple identical sensor elements (termed herein "sensor redundancy"), and the use of multiple sensor elements directed to the same target analyte, but comprising different chemical functionalities (termed herein "target redundancy"). For example, for the detection of nucleic acids, sensor redundancy utilizes a plurality of sensor elements such as beads comprising identical binding ligands such as probes. Target redundancy utilizes sensor elements with different probes to the same target: one probe may span the first 25 bases of the target, a second probe may span the second 25 bases of the target, etc. By building in either or both of these types of redundancy into an array, significant benefits are obtained. For example, a variety of statistical mathematical analyses may be done.

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In addition, while this is generally described herein for bead arrays, as will be appreciated by those in the art, this techniques can be used for any type of arrays designed to detect target analytes. Furthermore, while these techniques are generally described for nucleic acid systems, these techniques are useful in the detection of other binding ligand/target analyte systems as well.

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In a preferred embodiment, sensor redundancy is used. In this embodiment, a plurality of sensor elements, e.g. beads, comprising identical bioactive agents are used. That is, each subpopulation comprises a plurality of beads comprising identical bioactive agents (e.g. binding ligands). By using a number of identical sensor elements for a given array, the optical signal from each sensor element can be combined and any number of statistical analyses run, as outlined below. This can be done for a variety of reasons. For example, in time varying measurements, redundancy can significantly reduce the noise in the system. For non-time based measurements, redundancy can significantly increase the confidence of the data.

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In a preferred embodiment, a plurality of identical sensor elements are used. As will be appreciated by those in the art, the number of identical sensor elements will vary with the application and use of the sensor array. In general, anywhere from 2 to thousands may be used, with from 2 to 100 being preferred, 2 to 50 being particularly preferred and from 5 to 20 being especially preferred. In general, preliminary results indicate that roughly 10 beads gives a sufficient advantage, although for some applications, more identical sensor elements can be used.

Once obtained, the optical response signals from a plurality of sensor beads within each bead subpopulation can be manipulated and analyzed in a wide variety of ways, including baseline adjustment, averaging, standard deviation analysis, distribution and cluster analysis, confidence interval analysis, mean testing, etc.

5 In a preferred embodiment, the first manipulation of the optical response signals is an optional baseline adjustment. In a typical procedure, the standardized optical responses are adjusted to start at a value of 0.0 by subtracting the integer 1.0 from all data points. Doing this allows the baseline-loop data to remain at zero even when summed together and the random response signal noise is canceled out. When the sample is a fluid, the fluid pulse-loop temporal region, however, frequently  
10 exhibits a characteristic change in response, either positive, negative or neutral, prior to the sample pulse and often requires a baseline adjustment to overcome noise associated with drift in the first few data points due to charge buildup in the CCD camera. If no drift is present, typically the baseline from the first data point for each bead sensor is subtracted from all the response data for the same bead. If  
15 drift is observed, the average baseline from the first ten data points for each bead sensor is subtracted from the all the response data for the same bead. By applying this baseline adjustment, when multiple bead responses are added together they can be amplified while the baseline remains at zero. Since all beads respond at the same time to the sample (e.g. the sample pulse), they all see the pulse at the exact same time and there is no registering or adjusting needed for overlaying their  
20 responses. In addition, other types of baseline adjustment may be done, depending on the requirements and output of the system used.

Once the baseline has been adjusted, a number of possible statistical analyses may be run to generate known statistical parameters. Analyses based on redundancy are known and generally  
25 described in texts such as Freund and Walpole, *Mathematical Statistics*, Prentice Hall, Inc. New Jersey, 1980, hereby incorporated by reference in its entirety.

In a preferred embodiment, signal summing is done by simply adding the intensity values of all responses at each time point, generating a new temporal response comprised of the sum of all bead  
30 responses. These values can be baseline-adjusted or raw. As for all the analyses described herein, signal summing can be performed in real time or during post-data acquisition data reduction and analysis. In one embodiment, signal summing is performed with a commercial spreadsheet program (Excel, Microsoft, Redmond, WA) after optical response data is collected.

35 Methods for signal summing and analyses are included in U.S.S.N. 08/944,850, filed October 6, 1997; 09/287,573, filed April 6, 1999; and 60/238,866, filed October 6, 2000; an PCT Nos. US98/21193, filed October 6, 1998; and US00/09183, filed April 6, 2000.

Once made, the methods and compositions of the invention find use in a number of applications. In a

preferred embodiment, the compositions are used to probe a sample solution for the presence or absence of a target sequence, including the quantification of the amount of target sequence present. The compositions and methods find utility in the detection of genotyping assays and sequencing assays, and in all sorts of target analyte assays, including immunoassays.

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For SNP analysis, the ratio of different labels at a particular location on the array indicates the homozygosity or heterozygosity of the target sample, assuming the same concentration of each readout probe is used. Thus, for example, assuming a first readout probe comprising a first base at the readout position with a first detectable label and a second readout probe comprising a second  
10 base at the readout position with a second detectable label, equal signals (roughly 1:1 (taking into account the different signal intensities of the different labels, different hybridization efficiencies, and other reasons)) of the first and second labels indicates a heterozygote. The absence of a signal from the first label (or a ratio of approximately 0:1) indicates a homozygote of the second detection base; the absence of a signal from the second label (or a ratio of approximately 1:0) indicates a homozygote  
15 for the first detection base. As is appreciated by those in the art, the actual ratios for any particular system are generally determined empirically.

Generally, a sample containing a target analyte (whether for detection of the target analyte or screening for binding partners of the target analyte) is added to the array, under conditions suitable for  
20 binding of the target analyte to at least one of the capture probes, i.e. generally physiological conditions. The presence or absence of the target analyte is then detected. As will be appreciated by those in the art, this may be done in a variety of ways, generally through the use of a change in an optical signal. This change can occur via many different mechanisms. A few examples include the binding of a dye-tagged analyte to the bead, the production of a dye species on or near the beads, the  
25 destruction of an existing dye species, a change in the optical signature upon analyte interaction with dye on bead, or any other optical interrogatable event.

In a preferred embodiment, the change in optical signal occurs as a result of the binding of a target analyte that is labeled, either directly or indirectly, with a detectable label, preferably an optical label  
30 such as a fluorochrome. Thus, for example, when a proteinaceous target analyte is used, it may be either directly labeled with a fluor, or indirectly, for example through the use of a labeled antibody. Similarly, nucleic acids are easily labeled with fluorochromes, for example during PCR amplification as is known in the art. Alternatively, upon binding of the target sequences, a hybridization indicator may be used as the label. Hybridization indicators preferentially associate with double stranded  
35 nucleic acid, usually reversibly. Hybridization indicators include intercalators and minor and/or major groove binding moieties. In a preferred embodiment, intercalators may be used; since intercalation generally only occurs in the presence of double stranded nucleic acid, only in the presence of target hybridization will the label light up. Thus, upon binding of the target analyte to a capture probe, there is a new optical signal generated at that site, which then may be detected.

Alternatively, in some cases, as discussed above, the target analyte such as an enzyme generates a species that is either directly or indirectly optical detectable.

Furthermore, in some embodiments, a change in the optical signature may be the basis of the optical signal. For example, the interaction of some chemical target analytes with some fluorescent dyes on the beads may alter the optical signature, thus generating a different optical signal.

As will be appreciated by those in the art, in some embodiments, the presence or absence of the target analyte may be done using changes in other optical or non-optical signals, including, but not limited to, surface enhanced Raman spectroscopy, surface plasmon resonance, radioactivity, etc.

The assays may be run under a variety of experimental conditions, as will be appreciated by those in the art. A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding. Various blocking and washing steps may be utilized as is known in the art.

The following examples serve to more fully describe the manner of using the above-described invention, as well as to set forth the best modes contemplated for carrying out various aspects of the invention. It is understood that these examples in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references cited herein are incorporated by reference in their entirety.

### Examples

#### Example 1

##### Immobilization of Crude Oligonucleotides to a Solid Support

1. Introduce chemical functional group (such as -NH<sub>2</sub>, -COOH, -NCO, -NHS, -SH, -CHO, etc.) onto solid support.

2. Activate the functional group before oligonucleotide attachment.

3. 5'-terminal modified oligonucleotide attachment.

Crude Oligonucleotides were attached to supports and compared to results from attachment of purified oligonucleotides. As demonstrated in Figure 3, in the presence of 2M salt, crude oligonucleotides were immobilized as efficiently as purified oligonucleotides.

In addition, the improved attachment of oligonucleotides to a solid support in the presence of increased salt was sequence and length independent. Thus, the method finds use in attachment of all oligonucleotides to a solid support (see Figure 4).

In addition, when 0.5 M to 3 M NaCl was used for attachment of oligonucleotides, non-purified oligonucleotides were attached with comparable efficiency when compared to purified oligonucleotides (see Figure 5).



TABLE 1

Seq. ID No.	Decoder (5'-3')
17	GGCTGGTTCGGCCCCGAAAGCTTAG
18	GTTCCCAGTGAAGCTGCGATCTGG
19	TACTTGGCATGGAATCCCTTACGC
20	ACTAGCATATTTCAAGGCACCGGC
21	GAACGGTCAATGAACCCGCTGTGA
22	GCGGCCTTGGTTCAATATGAATCG
23	GATCGTTAGAGGGACCTTGCCCGA
24	TGGACCTAGTCCGGCAGTGACGAA
25	ATAAACTACCCAGGACGGGCGGAA
26	CATCGGTTGCGCCAATCCAGATA
27	GTCGGGCATAGAGCCGACCACCCT
28	CTTGGGTCATGATTCACCGTGCTA
29	TGCCTAACGTGCTAATCAGCAGCG
30	CGCATGTTGGAGCATATGCCCTGA
31	AGCCACTGCATCAGTGCTGTTCAA
32	GGTTGTTTGAGGCGTCCCACACT
33	TCGACCAAGAGCAAGGGCGGACCA
34	GACATCGCTATTGCGCATGGATCA
35	GAAATACGAAGTCTGCGGGAGTCG
36	TGTCATGAATGATTGATCGCGCGA
37	ATATCGGGATTGTTCCCGGTGAA
38	GCGAGCGTACCGAAGGGCCTAGAA
39	TTACCGGCAGCGGACTTCCGAATT
40	GTAATCGAGAGCTGCGCGCCGTCT
41	TCCCTGAGGTTCGGAAGCTTCCGAC
42	CCTGTTAGCGTAGGCGAGTCGATC
43	TAGCGGACCGGCAGAATGAGTTCC
44	GGTACATGCACTACGCGCACTCGG
45	AATTCATCTCGGACTCCCGCGGTA
46	GCCAAATCTGGATTGGCAGGAATG
47	TGCATTTTCGGTTGAGGCACATCC
48	CCGCTCAATTCACCATGCTTCGCT
49	CTCGGAAAGGTGCAACTTTGGTGT
50	AATTCGACCAGCAGAACGTCCCAT
51	GCCAGAGTCTCAACCTCACGGGAT
52	CCAACAACCTGGAACGGGAACCCGC
53	GAGAACTGATCGCTGAGGGGCATG
54	GGCACACTAGACTTGTGGCACCGA

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55	CTTGGGCAAACGCTTCAGCCACAA
56	TCACATCCAAATATGGTCCGCGAA
57	GTCTGCCGGTGTGACCGCTTCATT
58	CATCGCAGAGCATAAACACCCTCA
59	GTTGGTATCTATGGCAGAGGCGGA
60	ACGAGGTGCCGCTGAGGTTCCATT
61	GGAATGAGTGGACCCAGGCACATT
62	TGTCAATATGCGTCCGTGTCGTCT
63	TGATGAGCCTCAGGGTACGAGGCA
64	CACCGCGGTGTTCTACAGAATGA
65	TTGTTGCCAATGGTGTCCGCTCGG
66	TTAACCTGCGTCTGCCCTTTCCT
67	AGGCGCGTTCCTGCCTTAGTGACG
68	TAGGGCGATGGCACGAAGCTTCAA
69	TGCATAGAGCCAAAGTCGGCGATG
70	TTGAGAGGCAGGTGGCCACACGGA
71	TCCGCATTGTGAGAAAAACGAGC
72	GGCGGTTTCCGTAGCTATAGGTGC
73	GGTGAAAATTTCTAGCCACGGGC
74	CCGACGGAGGATGAAGACAATCAC
75	CCAGTTTGGCCCAATTCGCCAAAA
76	GGATCTATTAGGCCGTGCGCACAG
77	CGGATGTCACCGTTTGGACTTTCA
78	ATCGCAAATCCTGCTCGTCCCTAA
79	CAGGGCATGCAATAATCGAGGTTT
80	CATGCGTTGATATATGGGCCCAAG
81	CAGCTGCAGCTTGTGACCAACCAC
82	TTGTATGTCTGCCGACCGGCGACC
83	GATGGCGCCCGTTGATAGGTATGG
84	ATGAGAATCGCCGGCAATCTGCTA
85	ATTTGCACTGACCGCAGGCTCGTG
86	CAGGGAGAACGGTTAAGTTCCCGT
87	AGGCCGGCGATCGAGGAGTTTGGT
88	ACACGGTGGTCTCTGATAGCGACC
89	GTGCAACGCCGAGGACTTCCATCA
90	TCGGTGCCTGATAGCCATTCCGAT
91	TGAAATACCACACAGCCAATTGGC
92	GCATCGTGTACATGACTGCCGCGA
93	CAGTGTTCTAACGGCGCGCGTGAA
94	CGCTTGCAACGTTGCACCTACTCT
95	CGAAAACTAGTGGGCTCGCCGCG
96	CTTTCAGGGGAACTGCCGGAGTCG

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97	TTGTGGCCTTCTTGTAAGGCACG
98	TCCACGAACGGCGACCCGTTGTCT
99	CGACCTTGACGAAACCTAACGAG
100	GTGCAGCTTCACGAGCCAGCCTGA
101	CGCTTTCGTGCGAATAGACGATGA
102	TGCGCTTACAGGCTCCTAGTGGTC
103	CACGCGCTTAGTCGCGATCGCATA
104	CGGAGGGAGGGAGCTAGCCTTCGA
105	GCATCCGGCCTGTTGATGACGCCT
106	AGGCCAATCGATCTTATTGCCGAG
107	CCTTCCAATGATTGCATACGCCCA
108	AACACTTGATCAGGCGGGTCGTCT
109	TGGAATCAAGGCCGTAAAGGACAG
110	GCTCCCGTAACCTGTCCACCACTG
111	AGTGGTGAATGGCCGCTACCCTGA
112	TGTTGAAGCGAGCTAAAACGGCCA
113	CAGCGCTCCAGAATTGACAGCAAT
114	AAGGTGGTGCCATTCAATTTGGCTA
115	CGTTAAACCGCAATCCGTTTCGGCT
116	TGTCTTCCACCTCGAAGGTTTCCA
117	CACGAGATACCGGCGTAAGGGTGG
118	CTACGGCAAACGTGTGGAATGGGT
119	GTAGGGCGATGACGGGCGAACTAC
120	AATCGACCTCCGCACACATTTCGCA
121	GAGTCAGCATGGCGGCGGAGATTC
122	AGATAAAGACGCTGGCAACACGGG
123	GGTACCTCAACGCGAACCACCTTGT
124	AAGCGATGGCTACCCAAGAGCGAT
125	AGAGCTTATGCAGAACCAGGCGCC
126	ATCGGTCTCACGCAGGGTTGGATA
127	TAGGTTGCCCGCCAGAAGAAACAT
128	CGGTGCTGTTGCAAAAGCCTGTAG
129	TGATGAAAGTTTGCGGCAGGACAC
130	GTTGAGTGCAGGATGCAGCGATAG
131	AACATTGCGCGGTCCACCAGGGTT
132	GGGCAGTTAGAGAGGGCCAGAAGT
133	TCGAGCTGGTCCCCGTGAACGTGT
134	GTCTTGGGGGCCGCTTAGTGAAAA
135	ACTGTTGGCTTGCTCTCATGTCCA
136	AGGACCATTGGAAGGCGAAGATA
137	CTTGGGAGGCATCCGCTATAAGGA
138	AATAACGGAACGCACCGCTACAG

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139	TTGTACGTGCGGTCCCCATAAGCA
140	CGCACCAAAGTGAAGTTTCCCAGAC
141	ACCTGATCGTTCCCCTATTGGGAA
142	GGAACAGAGGCGAGGGGACTGAGC
143	CCCTGCCTTGGCGTGTGCGCTTAT
144	ACTCTGACACGCCAACTCCGGAAG
145	CTGACGGTTTTTCATTGCGCGTGCC
146	TGCGGTGGTTCATTGGAGCTGGCC
147	GCATGGCCAACTAGTGAAGTCGAA
148	AGGCCGTAAAGCGAATCTCACCTG
149	CGAATATTATGCCGAGAATCCGCG
150	ACAGACGAGCTCCCAACCACATGA
151	GGACGGTTTGTGCTGGATTGTCTG
152	AAAGGCTATTGAGTTGGTTGGGCG
153	GATGGCCTATTCGGAGATCGGGCC
154	GATCCAGTAGGCAGCTTCATCCCA
155	AATAACTCGCGCGGGTATGCTTCT
156	GGAGGAGGTTTGTCTCGGAAAGCA
157	CTTTGGTATGGCACATGCTGCCCG
158	AGAAAGGCTCGAGCAACGGGAACT
159	AATCTACCGCACTGGTCCGCAAGT
160	CGTGGCGGCCACAGTTTTTGGAGG
161	TTGCAGTTCAATCCATACGCACGT
162	GGCCCAAAGCCCCAGACCATTTTA
163	CGCCTGTCTTTGTCTCCGGACAAT
164	TGAGGCAACAGGGGCCAAAACTA
165	AGCGGAAGTAGTCCTCGGCTCGTC
166	GGCCCCAAGGCTTAGAGATAGTGG
167	GCACGTGAAGTTTAACCGCGATTG
168	AGCGGCAGAAACGTTCCCTTGACGG
169	TCGTGAGCAGACGAGATTGCACG
170	TCTTTGCCGCGTAACTGACTGCTT
171	TTTATGTGCCAAGGGGTTAACCGA
172	TGTTACTGTGGTTCACGGCAGTCC
173	CGCGCCTCGCTAGACCTTTTATTG
174	ACAAATGCGTGAGAGCTCCCAACT
175	CGCGCAGATTATAGACCCGAATGT
176	CAAATAACGCCGCTGAATCGGCGT
177	CCTTCGTGCATCGGTGATGATGTT
178	TGAACACGAGCAAACTCCAACGC
179	CAGCAGATCCTTCGTAGCGGTCGT
180	GGAACCTGGTGAGTTGTGCCTCAT

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181	TCATAAGCGACAATCGCGGGCTTA
182	CCCAACGTCACTGAAGCTCACAGT
183	TGTCAGAGCCCGCGACTCAGACGG
184	TACACGAAGCCTCTCCGTGGTCCA
185	CTCAGAAGTCCTCGGCGAACTGGG
186	ATCCTTTTATCTACTCCGCGGCGA
187	AGGCGTGACGCAACAGGATAAACC
188	ACTCTCGAGGGAGTCTCTGGCACA
189	TTGCCAGGTCCATCGAGACCTGTT
190	TCCACTATAACTGCGGGTCCGTGT
191	GCCCAGTCGGCTCTAACAAGTTCCG
192	CGGAACGGATAATCGGCGTCAGGT
193	TAAAATAAGCGCCTGGCGGGAGGA
194	GCGCACTCGTGAAACCTTTCTCGC
195	AGTTTGCCAGGTACTGGCAAGTGC
196	ACAACGAGGGATGTCCAGCGGCAT
197	TTCGCAGCACCCGCTAGGTACAGT
198	TAACCCGATTTTTGCGACTCTGCC
199	CGTCGCATTGCAAGCGTAGGCTTG
200	GAGCTGACGTCACCATCAGAGGAA
201	GGAGGCTGGGGGTGCGGCTTAAGT
202	TTGTGGGAACCGCACTAGCTGGCT
203	CCCTCGCACTGTGTTACCCCTCTT
204	TCATTGACTCGAATCCGCACAACG
205	ACAGGGGTTGGCCTTCGTACGTAC
206	AGGCCGTGCAACATCACACAGGAT
207	GGGCCGTGGTCACGTAATATTGGC
208	GCGCGGACATGAAACGACAAGGCC
209	CTTATTGGGTGCCGGTGTCCGATT
210	GGGGCGGTTACCAAAAAATCCGAT
211	GCTAAAGCGTGCTCCGTAAGTACC
212	ATCTCATGCATCTCGGTTCTGTCGT
213	ACGAAAAAAGTGTGCGGATCCCCT
214	CCAAGTACACCGCACGCATGTTTA
215	ATCGTGCGTGGAGTGTGCGCATCTA
216	TCCAGATACCGCCCCGAACCTTGA
217	TCTGCTGGCAGCACGTGAAGTGGC
218	TTGAAATTGCTCTGCCGTCAAGTCA
219	AGTCAGGCGAGATGTTCAAGGCAGC
220	ACAAGCCGACGTTAAGCCCGCCCA
221	CCCTAATGAGGCCAGTAACCTGCA
222	GTGAGACACACATCCCCTCCAATG

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223	CGACGGATGCAGAGTTCAGTGGTC
224	CCCGCATGCCTGGCGGTATTACAA
225	TTAGCAAAGCGGCGCCGTTAGCAA
226	CCCGACACGGGTCAGCGTAATAAT
227	GCGACGGCCCTGAGGTATGTCGTC
228	CAAAAGTGTGTTCCCTTGCGCTTG
229	TCTCGAAGCACAGCCCGGTTATTG
230	ATGCTAACCGTTGGCCATGGAAC
231	CTTGCGGAGTGTTAGCCCAGCGGT
232	TGCTCCCTAGGCGCTCGGAGGAGT
233	CCAATGCCTTTGAGTAAGCGATGG
234	AGCAGATAACGTCCCAATGACGCC
235	TTGACCATTACGTGTTGCGCCCAT
236	TCGCGTATTTGCGGAATTCGTCTG
237	CTGCGTGTCAACAATGTCCCGCAG
238	TCTGGTGCCACGCAAGGTCCACAG
239	CTCCGGGAGGTCACTTAATTGCGG
240	TTTTCGTGATTGCCCGGAGGAGGC
241	TCGGGATGTAGCTGGGGCTACCGG
242	CGAGCCAACGCAACACGTCCTTG
243	GCAAAGCCTTTGTGGGGCGGTAGT
244	ATTCGACCGGAAATGAGGTCTTCG
245	TTGCTTGCTGAGTTGCTCTGTTT
246	CGCGTGAAGACCCATTCCCGAGT
247	AACCGTATTCGCGGTCACTTGTGG
248	GGGGCCAACCGTTTCGAGGCGTAT
249	TTGCGCTGGCAGTCCAAACGGCTT
250	GGGTGTGGTTAGAATGCACGGTTC
251	GCGAGGACCGAACTAGACAAACGG
252	ACGCACGCGTGACCGAAGTTGCTG
253	TAAAAGGTCGCTTTGAAAGGGGGA
254	TGCGATCGCTAACTGCTGGGACAA
255	GGAGGTATAAGCGGAGCGGCCTCA
256	ATGCTGACATGTCGTGCACCTCGT
257	TGTGGTTAAAGCGTCCGTTCAACG
258	CGTTCACACCGGCGTAAGCTGCGT
259	CCTATCCCGGCGAGAACTTCTGTG
260	GTCTGCACTCACGCAGCGGAGGGA
261	GCACGAGTTGGTGCTCGGCAGATT
262	AACGTCGCACGACACAGTTCGTC
263	ATGCGCGCTTATCCTAGCATGGTC
264	TCACGTTTTCGTCTCGACATGAGG

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265	TGTGCCTCATCCTTAGGATACGGC
266	AGGTGGTGTGGGTCAACCGCTTTA
267	CTGGATCGAAGGGACTGCAAGCTC
268	TAGATCAACTCGCGTACGCATGGA
269	GATCCTGCGGAGAAGAGAGTGCAG
270	TACGTGTGGAGATGCCCCGAACCG
271	GCGCTATGTCAATCGTGGGCGTAG
272	AGCGAGGTTTCTAGCGTCGACACC
273	CGATGAAGACAGGTTTGCTGTTGC
274	ACCCAGGTTTTGCCGTTGTGGAAT
275	CCCTGTTAACGGCTGCGTAGTCTC
276	AGGCCGATTTACCCGCCAATTGC
277	GAGCCCTCACTCCTTGCCCTTTGA
278	GGGTGGACATCCGCCTCGCAGTCA
279	GATGGCTGAGAACCGTGCTACGAT
280	TCGACGTTAGGAGTGCTGCCAGAA
281	CGAATGGGTCTGGACCTTGATAG
282	GTGCACCAGACATTGAACTCGGA
283	AGAGGCCCGTATATCCCATCCAT
284	AACGCCTGTTTACAGCATCAGCGG
285	AAGGCTCAACACGCCTATGTGCGC
286	AGTCCGTGTTGCCAGATTGGCTCG
287	ATGTCCCATGTAAAGACGCGTGTG
288	ATGGAGTCTGCTACGCCCAAAGG
289	CGGCCTCCAACAAGGAGCACTAAC
290	CAGAGCCGTGGCAACATTGCGAGC
291	TCATTTGAATGAGGTGCGCACCGG
292	GACGTACCGGAAGCGCCGTATAAA
293	ATGCGAGCAATGGGATCCGGATTG
294	AGAGTGAGGCCTCCCTGACCAGTG
295	CGCACCGTAAGTAGATTGCCCCGC
296	AGGGTATCGGAGCCAGGGCTTACC
297	TGAACCTTTGAGCACGTCGTGCGC
298	TCCGCCTTTTTGGTTACCTCGAAG
299	GAACGCCAACGGCACTAACACATC
300	CCGACAGCAGCCAAGACGTCCCAG
301	TTGTACACCTGGGCCACGCACAGG
302	CATAAAAAACCTGGGGCTCTGCG
303	TGCCAACTGTGCAGACCGGACTTA
304	GGCGAAAGAGCGAAACCGGCTCGT
305	GGGATGCGTATTTTAGCGAACACG
306	TGGGATTCAGCGACCAGTACGCGA

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307	CCCGATATTCGCCCCGGCCTATTCTG
308	CGAGAAGATGCCTCACGCAACCAA
309	AACCTTGACCCGTGGATGACGCTA
310	GGCTAGACGATGGATACCCGTGCC
311	GCCTCTTCTCGACGATGCGATTTT
312	GCTTCCGGATGAACGGGATGGTTG
313	CCCTCCATGTTCTTCGAACGGTTT
314	TTGATGGGCGGCAATGCTCTTGCT
315	ATTGTGAGATGCGCCAAATCCCC
316	TCAGCACAGCCAGACGGTCAACTT
317	ACTCCACTCCTCGGTGGCAAATA
318	TCTGGGCATGCCTGGACGGAGACG
319	TCTCAACTCCGGTACGACGAAACA
320	TTGCGTGGTCAAAGGCGCAACGTG
321	AGACAGCGATCCGCGGCTCATGAT
322	CGCGTCTCTAACTGAGAGCAGCCA
323	AGGCGCACATGTACGGACATTCTAG
324	GATGAGTGGCACGTCGGTGTGTAA
325	TGATCCATATTGTCGGACGTTGCG
326	ACCTGCCGGGAGTTCATAGGCTAG
327	AGCATTGGCGTTTTTCCGCAACGA
328	GGTAATATTACGCGCGACCGCTCA
329	ATAGCGTACGACGAGGTGACGCGC
330	GGGTGAGGGAAAGAGCACCTGCCT
331	TAGGTCACGATGCGTTTGACGCTA
332	ACTGCCCCGTACCTCTGGTTCTGGC
333	CAAAAATCGGGTGAACATTGGCTG
334	CCTTTGGCCTGAAGTTGTCGTAGC
335	GTGCCCCACGAGCGTATCGTTGTA
336	AGGCGCTACGTGGGCCTGGAGCAA
337	GGGTGCTACCATTGCATTAGTCCG
338	ACCACGCGCGTACGTGTAACCGAG
339	CCATGATGCATTGGGTGCATTTAG
340	GGTCCGGCCCTACGAAACGTTCTGA
341	CCGTGTGGCTGGAGATTGCGTGTGA
342	GTTAGGGCGACGCATATTGGCACA
343	GGGTCAGTCAGGTGCGTTAGGATC
344	GCCGTGAAGTCGAATGCAGATCGA
345	GCCACCACCCAGTGCATTGAGGTA
346	GAGCTTAGTTTGCGGTCATCGGGC
347	TGTTTGCCGCCATTAGGGAGTAAC
348	GCTCCGCTGGATGTGCCGGTTTAG



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349	CGGTAGCATGCGAGATCCCTGTTA
350	CTACGCTCTACCAGTTGCCTGCGA
351	GTGCCTCCTGCTGTATTGCCAAG
352	TTGCGACTCGACTTGGACGAGTAG
353	TCTGGGAGCTGTTTACTCCAGCCA
354	TGCACGCGGAACTCCCTTTACCAT
355	TGGCAGCAAATGAATCGAAAGCAC
356	AACTGGTGACGCGGTACAGCGAAG
357	AGACGATTACGCTGGACGCCGTCG
358	ATGCCCTCCTTCATGGAAGGGTT
359	ATTCTCGGAGCGTATGCGCCAGAA
360	ATAGCGGAGTTTGGGTACGCGAAC
361	ACCTACGCATACCGCTTGGCGAGG
362	GATTACCTGAATGGCCAAGCGAGC
363	CCTGTTAGCATCACGGCGCTTAGG
364	CGGAATGATGCGCTCGACAACGCT
365	TGAGAGAGGCGTTGGTTAAGGCAA
366	AAGCAGGCGAAGGGATACTCCTCG
367	TCACGACAGACGGGCCGAGATTAC
368	AAGCAATTTGGCCTCGTTTTGTGA
369	GCTGGTTGCGGTAGGATCGCATAT
370	TTGTGAATCCGTTCTGTCCCCGAC
371	CTCCGATGACAATTGTGGAGAGCA
372	TGGGCTCCTCTGAGGCGAGATGGC
373	GGATAGAGTGAATCGACCGGCAAC
374	TGCACCGAACGTGCACGAGTAATT
375	GCCAGTATTCTCGGGTGTGGACG
376	TCGCTACCTAAGACCGGGCCATAC
377	TGGCATTGACGAGCAGCAGTCAGT
378	CGCGTCCCAGCGCCCTTGGAGTAT
379	ATGAAGCCTACCGGGCGACTTCGT
380	CCAGACAGATGGCCTGGAACCATG
381	TGGCGTGGGACCATCTCAAAGCTA
382	CCGCATGGGAACACGTGTCAAGGT
383	GCCCACTCGTCAGCTGGACGTAAT
384	ATTACGGTCGTGATCCAGAAAGCG
385	TGCGAGGTGAGCACCTACGAGAGA
386	GGGCCGCATTCTTGATGTCCATTG
387	CCTCGGATGTGGGCTCTCGCCTAG
388	TAGGCATGTTGGCGTGAGCGCTAT
389	CGATACGAACGAGGATGTCCGCCT
390	TACGCCGGTTAGCACGGTGCGCTA

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391	CATACGATGTCCGGGCCGTGTGCG
392	ATCCGCAGTTGTATGGCGCGTTAT
393	GGGTAAGGGACAAAGATGGGATGG
394	ATTGGAGTGTTTTGGTGAATCCGC
395	GAACCGAGCCAACGTATGGACACG
396	GCCGTCAAGCTTAAGGTTTTGGGC
397	ACCTGCTTTTGGGTGGGTGATATG
398	AATCGTGGGCGCAGCAAACGTATA
399	GTCGCCGGATTGCTCAGTATAAGC
400	ACCCGTCGATGCTTCCTCCTCAGA
401	ATCCGGGTGGGCGATACAAGAGAT
402	TTCCGCATGAGTCAGCTTTGAAAA
403	GCAAAGTCCCACTGGCAAGCCGAT
404	CGACCTCGGCTTCATCGTACACAT
405	CTCATGAGCGCAGTTGTGCGTGAG
406	CAGATGAAGGATCCACGGCCGGAG
407	TCAAAGGCTCTTGGATACAGCCGT
408	TCCGCTAATTTCCAATCAGGGCTC
409	ACGCACGGCGCTTTTGCCTTAATG
410	TGACAACGTCACAAGGAGCAGGAC
411	CTTAGTTGGGCGCGGTATCCAGA
412	GCTCTAATGCCGTGGAGTCGGAAC
413	CCGATTACAAATTGACTGACCGCA
414	AGACGTACGTGAGCCTCCCGTGTC
415	AATGGAGCGATACGATCCAACGCA
416	GGAGGCGCTGTACTGATAGGCGTA
417	TGTTTTTGAATTGACCACACGGGA
418	CATGTCTGGATGCGCTCAATGAAG
419	GCCCGCTAATCCGACACCCAGTTT
420	CCATTGACAGGAGAGCCATGAGCC
421	GAATCACCGAATCACCGACTCGTT
422	AACCAGCCGCAGTAGCTTACGTCG
423	TTTTCTGAGGGACACGCGGGCGTT
424	GGTGCTCCGTTTGATCGATCCTCC
425	CCGCTTAGGCCATACTCTGAGCCA
426	TAAGACATACCGACGCCCTTGCCT
427	GTTCCCGACGCCAGTCATTGAGAC
428	TAAAAGTTTCGCGGAGGTCGGGCT
429	CGGTCCAGACGAGCTGAGTTCGGC
430	CGGCGTAGCGGCTACGGACTTAAA
431	GCTTGGATGCCCATGCGGCAAGGT
432	AGCGGGATCCCAGAGTTTCGAAAA

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433	GAGCTTGAGAGCGAGGTCATCCTC
434	GCATCGGCCGTTTTGACCATATTC
435	CATAGCGCTGCACGTTTCGACCGC
436	ACCCGACAACCACCAATTCAAAAA
437	GCGAACAATCATAAGAGCGCCCTG
438	TTTTGGTGTGGCCGTTGAAGCTC
439	CCGCCGAGTGTAGAGAGACTCCGA
440	GACATCGGGAGCCGGAACATGAG
441	TCGTGTAGACTCGGCGACAGGCGT
442	ATGCGCATATACTGACTGCGCAGG
443	ACAAGCGAACCCGAGTTTTGATGA
444	GCATGAGACTCCGCGAAGACATGT
445	TCCTACATGTCGCGTCACGATCAC
446	GACCGATCGCGAAGTCGTACACAT
447	GTCGCCAGGACTGGGCCGATGTGA
448	ACCGATAAGACTTGCATCCGAACG
449	TCCATAACCAGTCCGAAGTGCCGG
450	ACGCGCCCTGCATCTCGTATTTAA
451	AGACCGCATCAATTGGCGCGTACC
452	AGAGGCTTGGCAAGTAGGGACCCT
453	GCAATGGACGCCAGACGATACCGG
454	GCTGGACTTAGTCGTGTTCCGGCGG
455	GGGGCTCATGAACGAAAGGCCTTT
456	AGGCATCGTGCCGGATTGCTCCCT
457	TGCGCATGTGACGTTGAACAAAG
458	ATTGCATTATGCGGTCCCTCAAAC
459	TTCGGGTCACATCCGATGCCATAC
460	ACCCATCGCCGAAAGCGATGTTG
461	AAGCGCTGACTCGGCTAAGAATCA
462	ACTTCCAAGTCCTTGACCGTCCGA
463	TCTCAATATTCCCGTAGTCGCCCA
464	AACAGTTCCTCTTTTCTGCGCGC
465	CGTCTCCATGTTGTACGAACAG
466	TGCGCAGACCTACCTGTCTTTGCT
467	ATGGACGGCTTCGCAGTCCTCCTT
468	TGAACGCTTTCTATGGGCCACGTA
469	TGAACCCTGCCGCGAGCGATAACC
470	GTTCTTGCGCGATGAATCAGGACC
471	AGGGTACGTGTCGCAGCTTCGCGT
472	ACCCTTGCTCCGCCATGTCTCTCA
473	GGGACAAGGATTGAAGCTGGCGTC
474	TGTCGTTGCTCCCGAGTACCATTG

475	GTGGTTATCTGCGAGGGCTTTTGA
476	GTTGTCCGAGACGTTTGTGTCAGC
477	GCTGGTGAACACTCACGAACCGCT
478	GCAGACAGGGCAAATCGGTGCAAA
479	CCCATCACAAACGAGTGGCGACTTT
480	GCTTCTACAGCTGGCGTGCTAGCG
481	GAATGTGTGCCGACCATTCTAGCC
482	CCAGCGGAAGTTAGAGCTCTGTGG
483	TTTTTACCGACCACTCCATGTCGG
484	GCGGCTATGTGATGACGGCCTAGC
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486	TCCTGTGTGGTGGCGCACTCCAC
487	CCAACTAACCAATCGCGCGGATGA
488	AGTGAGTGACCAAGGCAGGAGCAA
489	CATCTTTCGCGGAGTTTATTGCGG
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491	CTCACGAAAACGTGGGCCCGAAAT
492	CGCAGCAGCTGAACTCTAGCATTG
493	AGGAGACATACGCCCAAATGGTGC
494	ATTGAGAACTCGTGCGGGAGTTTG
495	CTCTTTGTAGGCCAGGAGGAGCA
496	GCCGCAGGGTCGATAATTGGTCTA
497	AAACGCCGCCCTGAGACTATTGGG
498	CTGAGTTGCCTGGAACGTTGGACT
499	CGGATGGGTTGCAGAGTATGGGAT
500	CTGACCTTTGGGGGTTAGTGCGGT
501	GGAAATGAGAACCTTACCCCAGCG
502	AACGCATCGTCCGTCAACTCATCA
503	TGGAGAGAGACTTCGGCCATTGTT
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505	TTGCGCTCATTGGATCTTGTGAGG
506	AGCGCGTTAAAGCACGGCAACATT
507	AGCCAGTAAACTGTGGGCGGCTGT
508	CGACTGATGTGCAACCAGCAGCTG
509	GGTTGCTCATACGACGAGCGAGTG
510	GCGCAAATCCACGGAACCCGTACC
511	ACGCAGTTTATTCCCCTGGCTTCT
512	AGAACCTCCGCGCCTCCGTAGTAG
513	AAAGGAGCTTTCGCCCAACGTACC
514	AGTGATTGTGCCACTCCACAGCTC
515	GCGATCGTCGAGGGTTGAGCTGAA
516	GGGAGACAGCCATTATGGTCCTCG

517	GAGACGCTGTCACTCCGGCAGAAC
518	CCACCGGTCGCTTAAGATGCACTT
519	CGGCATAACGTCCAGTCCTGGGAC
520	AAGCGGAACGGGTTATACCGAGGT
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522	AGGGAACCGCGTTCAAACCTCAGTT
523	GAATTACAACCACCCGCTCGTGTT
524	TTCAGTGCTCACGAAGCATGGATT
525	TTAGTTTGCGGTTGGGACTTCACC
526	AATGCGACCTCGACGAGCCTCATA
527	CCGAAACCGTTAACGTGGCGCACA
528	TAAAGTAACAAGGCGACCTCCCGC
529	TAATGATTTTAGTCGCGGGGTGGG
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531	TGGCGGACGACTCAATATCTCACG
532	GGGCGTTAGGCGTAATAGACCGTC
533	GCCACCTTTAGACGGCGGCTCTAG
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535	CAACCTCGTTGTCGAGTTTCTCGG
536	TAGCTCGTGGCCCTCCAAGCGTGT
537	GTGTCGGCGCTATTTGGCCTTACC
538	CCAGGGAAGCAACTGGTTGCCATT
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543	AAGATCTGCGAGGCATCCCGGCTT
544	GCAAGTGTATCGCACAGTGCGATT
545	CCGACAAGGCCTCAATTCATTCTG
546	GTCTCGTCTCAACTTTAAGGCGCG
547	ATCCAGAGATCCGTTTTGCAGCGT
548	GTCACCAGGAGGGAAGTTTCACCC
549	TATCTTACGCCCCACGGTCGAGCT
550	TTCCGTCAGGCGGATCAACGGAAT
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552	TGGGCCGCTTGGCGCTTTCATAGA
553	CCTAGCGCGAGCTTACTGACCAG
554	TTGGCCAGGAATATGGTCTCGAGA
555	GTCTGCGGCCGACTTGCTATGCAT
556	AACTTGCTCATTCTCAAGCCGACG
557	ACGTCAGCGATTGTGGCGAAATAT
558	ACGGCCTGCGTCAGCACATGCATC.

559	ATACCTCCGCAGAACCAATCCGTT
560	AGTTCGCGGTCCCACGATTCACCT
561	TGCTCAATTTGTGCAGAAAACGCC
562	TTATCGCGAGAGACGACCGTGTCC
563	GACGCGACGTGAGTAGTGAAGCG
564	ATGGTAGGGGCATTGGGCTTTCCT
565	CCAAATATAGCCGCGCGGAGAÇAT
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567	TAGCGTCTTGCGTGAAACCATGGG
568	CCACCCCGACAGCGCTGGACTCTT
569	ACGAGCACTGAAGGCTGCTTTACG
570	CATATCAGCGTCGTCTAGCTCGCG
571	TGATCCCGGACCGGCTAGACTAAT
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573	GGCTCCAGGGCGAGATTATGAATG
574	CAAAATCCGATGGGCGGAAAATTA
575	CACAGGCGCATAGGGAGCAAGCTA
576	TAGCTATTGCCCCGATGGGCTACT
577	TGGTACGCGGTCCATAGCAAGTCG
578	GACGCTGTGGCTCGGAAACTGTTG
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586	TCTCAGTCGGACTCGTATGCCAGA
587	CTCCAAACGCACACATCAAGCATC
588	TTCAACCAAGCGGGGTGTTTCGTGA
589	GGTGTGCGAGGGTGGTGACCTCGA
590	AGCGCTTTTGGTCATGATTTGCAA
591	CCGAGGACTTACGTCTGCCAGGA
592	GCCCAATCCAGTTCTTATGCGCCC
593	AAGCTTTGCGAAAGGTGTGTTGGC
594	CGGGTTAACCCACGCAAGTTATGA
595	TGATTAGCGCTCAATACACGCGTG
596	AAGGGCAGACCTTTGGTTCGACTG
597	GCGCCACAAGATTCACATGTCATT
598	GCCATGTTCAAGGGCCTTTCGAAG
599	CGCGGTGTTTTGTCTAGGTGCCGG
600	CAACATTGTGGTGGCACTCCATCC

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601	CGATACGCGCCGGTTTGTTAAATC
602	GGCTATAAACGTGCGGACTGCTCC
603	TGGGTAAATCACTATTGCGCGGTT
604	GTCTTCATCGGCCCGCGCAAGCTA
605	GCGACACACCCTGTACTCTGATGC
606	GTAGCAGGGTCCGCAAGACCAAGC
607	TCGCCAACGCAGGGTAACTGCCAT
608	ACTCCGAAGCTTCGAGCGGCACGA
609	TCCCGCCCACTAGACTGACTCGTA
610	ACCTTCTGGGGTCGCTCACCAATA
611	ATCATCCACGGCAGAGTGAAGAG
612	CGCTGGACTGGCCTATCCGAGTCG
613	CGGTCTCAGCAACACTGTGCGAAA
614	CGAACGTTCTCCGATGTAATGGCC
615	ATACCGTGCGACAAGCCCCTCTGA
616	AGCTCATTCCCGAGACGGAACACC
617	TTTCATGCGGCCGTTGCAAATCAT
618	ACTCGAACGGACGTTCAATTCCA
619	CTGCATGGTGTGGGTGAGACTCCC
620	CCGCGAGTGTGGATGGCGTGTTGA
621	AATGTGTGGTCTTAAGCCGGGTG
622	TAAGACGAGCCTGCACAGCTTGCG
623	GGCGTGGGAGGATAAGACGATGTC
624	TGCTCCATGTTAGGAACGCACCAC
625	CGGTGTTGGTCGGACTGACGACTG
626	CCGCGCGTATCTATCAGATCTGGG
627	AAAGCATGCTCCACCTGGAGCGAG
628	ACTTGATCGCTGGGTAGATCCGG
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630	ATGCAGATGAACAAATCGCCGAAT
631	GCAATTCTGGGCCATGTATTGTC
632	AGGGTTCCTTACGCGTCGACATGG
633	GTGGAGCTAATCGCGAGCCTCAGA
634	TCGTAGTCTCACCGGCAATGATCC
635	TTATAGCAGTGCGCCAATGCTTCG
636	CGAACAGTGCTGTCCGTGCTCAA
637	TCCGCGTGGACTGTTAGACGCTAT
638	CATTAGCCCGCTGTGCGTAACTGT
639	GGAAAGAACTCAGACGCGCAATG
640	CGACTCGCTGGACAGGAGAATCGT
641	CATGATCCTCTGTTTCACCCGCGG
642	GGCGTAGCGCTCTAAAAGCTTCGG

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643	AGTGATGCCATCAGGCCCCGTATAC
644	TATGGAAAGGGCAACAGCGCTATC
645	CTGTGGTTGATGGAGGATCCACAC
646	ACTCGCTGGAATTTGCGCTGACAC
647	CAGGCCCCGAACCACGCGGTTACAG
648	GGCGCAATGGGCGCATAAATACTA
649	GGTCAATTCGCGCTACATGCCCTA
650	TGAGGGCTGTTTGGTATTTGACCC
651	GATGGTGGACTGGAGCCCTTCCGC
652	CCGCGCATAGCGCAATAGGGGAGA
653	TCTTCTGGCTGTCCGGCACCCGAA
654	GCGTTCGCAATTCACGGGCCCTTA
655	TCGTTTCGGCCTTGGAGAGTATCG
656	AGGTGCAAGTGCAAGGCGAGAGGC
657	CGCCAGTTTTCGATGGCTGACGTTT
658	GCTTTACCGCCGATCCCAGATATC
659	GTGCTTGACGAAGAGGCGAAATGT
660	CAGTCCGTGCGCTTCATGTCCTCA
661	TACGCGTAAGAGCCTACCCTCGCG
662	GGCGAGTCTTGTTGGGGACATGTGT
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665	AAATCCGCGATGTGCCGTGAGGCT
666	GGCTTCGCACCCGTACCAATTTAG
667	TGTAGAGTCCCACGTAGCCGGCAT
668	CACTAGTCTGGGGCAAGGTGCATT
669	TGTACTCGGCAGGCGCAATAGATT
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671	CGGACTGCCCGTTTGCAAGTTGAG
672	ATCGTTCAGCACTGGAGCCCGTAA
673	ATGCATCGAACTAGTCGTGACGGC
674	TTCCAGGCATTAAGGAGAGGGAGC
675	GTGCGACATCTACTCCACGATCCC
676	CTCATCGTCCTAACACGAGAGCCC
677	AATGGCACTTCGGCGGTGATGCAA
678	CCGTGGGAGGGAATCCAACCGAGG
679	AAATTCTCGTTGGTGACGGCTCAT
680	TTGCTCTTATCCTTGTCTGGGCG
681	TTAAGGATCAGGCGGAGCTTGCAG
682	CGCGACTAAGGTGCTGCAACTCGA
683	GCTCGATTTACGGCCCGTTGTTC
684	AGCAGAGTGCCTTGCGAGAGGCTAA



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686	AACCGTTTAGGGTACATTGCGGGT
687	TATGATCGCTCGGCTCACAGTTTG
688	GACTTTTTGCGGAAACGTCATGGT
689	TGTCGGTTATTCCACCTGCAAGGA
690	CTATGGTTTGCACTGCGCCGTCGA
691	AGCAGGGAAATTCAATCGTTCGCA
692	CCTAACCGAGCGCTTAGCATTTC
693	CCCGACCCTAACTCGCATTGAATA
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704	TGTCAGCTGGTAGCCTCCGTTTGA
705	AGCGTCGCATGACGCTTACGGCAC
706	TCACTCAGCGCTGTGACTGCCTGA
707	GTTTGCGCTATAGTGGGGGACCGT
708	GTCGCATTCTGCACTGGCTTCGCC
709	TGATTAGGTGCGGTCCCGTAGTCC
710	AAGGGACCTTGGGTGACGGCGAGA
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712	CTCCGACGACCAATAAATAGCCGC
713	GGCTATTCCCGTAGAGAGCGTCCA
714	TGGATAACCTCTCGGTCCATCCAC
715	GACCGCTGTACGGGAGTGTGCCTT
716	GCCACAGAGTTTTAGCAGGGACCC
717	CCCACGCTTTCCGACCACTGACCT
718	CATTGACACAATGCGGGGACTGAT
719	AGCCACTCGACAGGGTTCCAAAGC
720	CAGGATGAGCAAAGCGACTCTCCA
721	CAAGGTATGGTCTGGGGCCTAAGC
722	GGTGTTCCGGCCTAACTCTTTCGG
723	TTTAGTCGGACCCTGTGGCAATTC
724	CACACGTTTCCGACCAGCCTGAAC
725	CTGGACGAACTGGCTTCCTCGTAC
726	TTCACAATCCGCCGAAAACGACC

727	AACAGGATATCCGCGATCACGACA
728	TACGTCGGATCCATTGCGCQAGT
729	CATGGATCTCTCGGTTTGATCGCC
730	AGCCAGGCGCGTATATACGCTCGG
731	ATTTGGCACGTGTCGTGCCATGTT
732	CCGCGTTGCACCACTTTGAGGTGC
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734	CTGAATCGCGCAAGTAAATGGGGG
735	GATAAGGTCCACCAGATTGCGCGC
736	CTAACAAATTGCCAACCGGGACGGC
737	GGTAACCTGGGTGCTTGCAGGTTA
738	ATCGGAGCCACCATTGCGATTGGG
739	GTGAACTGGCTTGCCCCAGGATTA
740	AGGCGATAGCATGGTCCCATATGA
741	AACGGTATCGTGGCTAATGCACGA
742	AGTAGTGGTCCTCCAGATCGGCAA
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747	CAAGGCGAGTCCACTCGAGGGGAC
748	GCAACTTGACGGCATAAGTGGCC
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754	CACAGATGGAGACAAACGCGCCTT
755	TTTTCGCAACTCGCTCCATAACCC
756	ACGTTACGTTTCCGGCGCCTCTAA
757	TATCGGATTGCGTGGGTTTCAATC
758	CTTCCACAATTGTCTGCGACGCAC
759	TGCACAAAGGTATGGCTGTCCGGC
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761	TCCGATGCCAGTCCCATCTTAAGA
762	CTGAAACCGTGCGAATCGAGGTGA
763	CGGTGTTCCGCGTGTGAAAAAAT
764	TCTAGCAGGCCTTTTGAATCGCCA
765	GAGTCACCTCTGAGACGGACGCCA
766	TCTTCTGTGTCATCCTGCAGCAGCAT
767	GCGGATGAAACCTGAAAGGGGCCT
768	GGGGCCCCAACTGGTATCAAGCC

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769	GCATTGGCTTCGGATTCTCCTACA
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772	ACGATGAACATGAATCGGGAGTCG
773	CTGCATCCCTGTAGCAGCGCTCCG
774	GTGCCGTATTTGACCTGTGCGTT
775	GCAGTGCGCACTTCAGTTCAAAAG
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779	CCCCTTACGGCTCGTCGTCTATGC
780	GCGCTTGCCCGATGCGATGCATTA
781	TTTCTGTAAGCGGCCTGGGGTTCA
782	GGCTGAGGTGAGCGGTAAGGATGA
783	TCTTGGCCTCCCCGATCTAATTTG
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785	GTAATCCATTTGTGGCTGCGTCAA
786	CAAACCCATTCCAGCAGACGCCTG
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789	GCAAGTGCTTAGCTCGTCAGCCTC
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791	CTAACGTCGTCTCGCGCAATCACT
792	TTTTCATAAACGTTGTCCCCGAGC
793	AGCAGGAGGACGAACCTCCGCTCC
794	TTCAAGCACCATCGTGCAATCCAA
795	AGCGTCGCCAGTGATCGCTAGTGG
796	TACATTCCCTGCCTCCGTGGGCTT
797	CGCTTCGCGTATTAGTAGCGGTT
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799	TCTGAGCAGGCCAGCGCTCCAGCT
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804	ATTGGCCGAGGGTGAATGCAGCCT
805	TGATCCATCCGAATGCTTTTCCAT
806	GCACACAGTTGTCTTGGCCCATGA
807	CTGGCGGGCAGTGGA AAAAACAAC
808	ATCTCCATGCGTAAGACTGCTCCG
809	TCTCCTCTCGTCGCAGTTCGTGGA
810	TAGCGTATTCACTCTTGCCGAGCA

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811	CAATCAAAAGCCACGGCGCGATGG
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814	TAGGCACTGCCGGTTCAGATTCAA
815	AACAGGGTGATAACGGTGGCCAAT
816	CGTGCGTACCATGTGTAAGTGCGT
817	GACCAATTCTACTTCGGCAGCCCA
818	ATCGGACCGATTTGCTTTTGGCTG
819	TCCGCCGAAGCACACGCTTATTCG
820	AACGGTACGCATTGTGAGCAGTGT
821	TGGCGACTACTGTTCCCCTGAATC
822	CAGAGGGGACAGCCGTATGCCTTA
823	CGGTGGTTTTATCGGAATCTGCCA
824	TTGGCCTCCGACCTCACGACATAT
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826	ACTAAGCGGTGGAGCCGGTGGATG
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829	GTTGCATGTGGCTCAGGCGGCATA
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831	CTCTCCAAGGAGACGAGCCAATGT
832	GAAAGGACGGGATTTGGGGGCTAA
833	TATGTAGTACCTTGGCTCGCGCCA
834	TCCCTTTCGATGAGCGGCTGTACT
835	TAGATCGGGCAGAGCCCGTATCTT
836	GGAATGCTTTAGGCTGCCGAGCTG
837	ATGGTAGCAACATTCAACGCCAGG
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839	ATGTTGCTAGTGCCCTTTCGGGCCT
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841	GATAGTGCTCGAAACGGGCCTTC
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843	GGCGTGAATAGAGTGACCAGGCGG
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858	TTGCGGAGATGCGACGGTACATTG
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862	GAATTTGGAACGGTGTCCGATGA
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868	TGGGGTTTCGTACAGGTCCGGTTCAT
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874	ATGCTCAGGTGCTAAATACGGCCA
875	AAAAATGTTTAGCGCGCTGACTGG
876	ATAGTCCGTTTCCGTTCCCAACGA
877	TCGATCTTCTGGGTTCAGACCAG
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887	TGGTACTCCTTGTCATGCCTGCCA
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889	GAATCTGGGCATTGCTACGAGACC
890	CGAAATGGGAGCGTCCACTACCAC
891	ACATATGAGCTCGCGTGCTTGCAT
892	TCGAGCACGGTCACTGATAAAGCC
893	GAGGGTCCCTGCTCAGAGTTGGTT
894	AAATGCGATCGCCCCTTATGGAAT

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895	CTACCCGAATGGATTGCGGATGGC
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898	GGCCGCACGTACGATTACGCCTTG
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904	AATTGTCCGCCAAACGCTTTTCAG
905	GTCGGCTTCGAGCGATCGAGTGTG
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907	GGCTTCCGCGATAACGTAATTCGC
908	TGTAGCCGACTAGGGCCGAAGCCC
909	AAGCGAACGCCCTGGCTGAATATT
910	TGTCACGCGACGTGCTGCAGATTT
911	CCGTGTCCGTGTTGTCGACAGGCG
912	CCCCACACGTTGCGCCTATATGTG
913	GGCGGGCACAACCTCAACACAGATG
914	CGACTGCGGGATCACCGGTGATTA
915	TCGGGACATGACCGGTACGGAGTC
916	TACCTCGAGTGGCCGTTGATCGGG
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918	ACACTCTAAGCCGATTCCGTTCTGA
919	GTGGGCGTGAGTGACACGCACAAA
920	ACGACTCCTCGGGCAAAGTACGTA
921	TGTGGTCATGGCGCTACTGTTTTCT
922	CTTTCGCTAGCCAGAGCGGGTTCC
923	ACAGGGCGTGTTAGCGTGTGACAA
924	GGTACTCCGGCGTATCGGGCCAC
925	GTGGGTTTTGTTACCCCTTCTGGG
926	ACGCAATTCCGCATTACTTACCCG
927	CGCCTCGACTGCGGTCAAGCACAA
928	GTGAAATGGATCCAGAGAGGGCCA
929	TATAAACGCTGCAGGGCTCCGTTA
930	GTTATTCAGGCGGCTTGTAACGGG
931	GGGTTCTAGCGTGCGCGTTCAGTT
932	TTGGGCTCGAGCGGTACACCACTA
933	CCGTCTTCAGGACAACGGTATGCG
934	GGACCCTTTGACAGATTGCGGCAC
935	TAAATTTTATCGCCAGGCGGCGCT
936	GCCGAACGCAAGATCGCTTGAAC

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937	TAGGCCATTGGTGCCCTAAGACGG
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940	TAGCGCGCATCACACTTGAATCG
941	TGCTGACACAAACGAGCCGTTTCG
942	CGCTTAACGGCATTGACTGTCCAC
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944	TTTATGCCGTTGCCGAGGAAGACT
945	AGTGCCGAGATAGGGGACTGGGCG
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949	ATATGCGTCACCACCCGGTCCGA
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957	GCGGGCGATGCTCCTTAAAGGGTA
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962	GCTTGAACCTCGAGGCGATGTTCT
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965	TCCCTGGGCTAGCATTGCGAGGTT
966	AGAACCAGACGCTTGTTTGCCG
967	CGTCACATGCAAACGTTCCCTCCC
968	TGACCGCATGTGTATTGAGTCGCT
969	GCGGGCCCAATGAGTATCCGTCAT
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971	GGCACCCTGCGCGCGTATATC
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983	GCGTACATCTGCTCATCAGCATGG
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990	GCGCCCTCACTGCATTTTGGTAT
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1127	CTTATCCCATGTGCCGGTCTGACT
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1176	CACAAGCGACATTTCTGGTGCACG
1177	CCAGAATGCGTGAATTCGCGTCCT
1178	CAAGGGAGCCCTGCGAATTAGAGT
1179	ATTCTTGCTTCGGACGACTAGCCG
1180	TGCCACTTTGATTTCCAGATTGCC
1181	GATGGTCGGCAGATAAGTGGTGGG
1182	GTTACACGCGGTTGACCAACATGT
1183	GATTCAATTGCCCCATTCTGCAT
1184	TACCGGAAACTGAGCCTCGTGCTA
1185	GGATCTTTACTCAGGGGCAGAGCC
1186	CGCGAGTGCTTTGTTCTGTGTGGA
1187	GTCGTGCGATGGCGTACATCCTT
1188	ACGGGAATCTCCCGAAGTGCGAGC

1189	GGTCGAAATGAGCCAGCAGCAGAT
1190	CCATTGGAATACTGCGTGCGGCTT
1191	GGAAGACTTCGCGAGGGCACAATG
1192	AGGGTGACTTCGAAGGTCCGAACT
1193	TCGTCCCTCTGGTGGTCAATCAC
1194	TGTGCAAATTATGCTGGGCGTGAG
1195	GTCGCCAACTGTCATGTGTGCCCA
1196	CCTCGAACCCCTCAAGACGAAACGA
1197	CTTCATCACGTGACCTTTGTTGCC
1198	CCTTCATTCCCAGCAGGATGGCTT
1199	CGGGGACCTCAATGGAGCGTCTTA
1200	CGCCTCTAGCGCTTGTTACGTCGA
1201	CTGCCAGACTCAAAACAGGGACGG
1202	CTCCTTACACCGTGTGAGGGAACC
1203	TTTCATGCCATATCGCCTCGCGCA
1204	TCTGGCTTTTCCTCGATCAATCGT
1205	GTCTGACTGTCTGCCCTGTATGCG
1206	GGTTAATGGAACGGCGTTAACGCG
1207	CTTCGCACTGCGGAATCTCAAGCT
1208	TGCCAGAGGCGTAGGAGTCCTGGA
1209	GACGGGCGAGCCAGTATTAACCTCA
1210	GACCTCCAAAGTCAGTCTTGCGGG
1211	CGTTAGAGCATGACCGAACACGTC
1212	GTGGGCTCAAAAATTGGGTACGCC
1213	GGGGCAGAGATCACGCGTTCCTCT
1214	TTTCGCCCTACGAAGCGAAGTTTC
1215	TACGGGGTGATGTTAAGCTACGCG
1216	CCTGTGAGTCTGAGATCGCCGTGT
1217	ACTGAAGCTGGAACAGGCCATTTCG
1218	AGCACTGGTTCACATGGGAGTCCA
1219	TAAGGAAGATCACACTCCCTGCGC
1220	CACCACACGCTAAAATTGAAGCCG
1221	GCTGTCGCCAGGATCATGTATCGT
1222	TTCGTTCTGTCAGTGGATTCTTGA
1223	TCAGCTCTCCTTGCTTGCACTG
1224	ACGACGAGGTGAACTTCGTGGGAA
1225	AGCATTGCCGCGGGCCTTGTTTA
1226	CAGAGGGCAGATGTGACTCCTCAA
1227	CGATATTTAGCCTCTCAAACGCG
1228	TGCCAGAAATGTTGCCGATTGAA
1229	TAGGCCACCCGGTGTTACAATTC
1230	GAGAGTCAGACCGAGGGACACGAG

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1231	GAGGCGATCCTGGAACCACGCAAC
1232	CCAGAGAGGCGGGCTACTGACTCA
1233	CACACAGTCCCATCGTACGGCAGT
1234	TTACGTTGCGGAAGCGTGCCTCTA
1235	ATGTACACGCTGCAATCGTGTCCT
1236	ACTCGTCGTCGGAAGCGCCAGGT
1237	ATGCGAGAGCAGAATTGAGCCGGT
1238	AAGTTGGTTCGTATTCACGCGTGC
1239	TGGGCTTATCGCCGAAGATTGCTA
1240	CAACGGCGAAGACCCAGAATTTTA
1241	AGCGTACGGCGAAAGTCTAGGGAC
1242	ATGCATCCAGCGTCCCCTTGATTA
1243	ACCGTCATCAGTCGCAGGCTTCTG
1244	TCTTGACGGCTGGGCATGATTGGA
1245	TTAACATTTCGGACCCAGGACCTGG
1246	TGGTGTGCGAACTCCCTTGCGTGTT
1247	TACTCCAGTCGCCTGCGCGCAAAC
1248	CGCAATGCCGTAAGCATGCCAAGC
1249	AGTCCGCGCGAAATACGAACAGTA
1250	ATGTTGCACGCGCACTGTATCACA
1251	GGGATCAGCATCATTGGAAAGGAG
1252	ATCGCCTAACTACCCGCGGCGTGC
1253	TGGCCAGGGAACACAAGCTCGGTA
1254	AAACATGGGTCGCGTCTGAGATCA
1255	GCGAGAGCTGCGATTCCCTTTTAG
1256	CCGGCCAAACAAGAGACGAGCGGA
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1258	TGTCTCGGGCCTTCAGGACACACT
1259	TCCACCTTCATTAAGTGGTTCGGC
1260	GCTTCGGAATCATCCACCTGTCAT
1261	GAGCCGATGGGCTATCGTCGTCGG
1262	CACGAATTACGCACGCACAGAGGA
1263	GCTGTGACGCTCCCCTCAACTAGG
1264	CGCTCTGAAAACGCGGGCTACGTT
1265	GAGTGCTGGACACCGTAGCCAGGA
1266	CCAACCCAGTGTAGGCGCAAATG
1267	GAAGTAGGGGATGTTGGCCGGCGG
1268	CAACGTGGGCACCTGTTTAGCAG
1269	CTAGCTGCGATCCGAACCTCTACG
1270	CATTGAACCATCAGCCAAGCTGCG
1271	AGACTGGCAATTTTCGAGGCCAA
1272	CTGGCCGTCCATGAGTTGGTCCAG

1273	CATGCTGAAACACGGGATTGCCAT
1274	CGATATGTAAGACAGCCGTCGCAA
1275	AGCGTAACCTACTGGGAAGGCACC
1276	GTGCTCGTGGCACGTACAGGCCTT
1277	GTTCGAACCCCGCGATGTTAAATG
1278	GTTGTTAGGAGGCTCGAGGCTGCT
1279	ACTGGTGCTACGCGGGATATTTGA
1280	CTGGGAGCTATCCTCAGCCGAATC
1281	GAACTCGCCGCTGCCGAAGGGTAG
1282	TTCGATCGAGGAGCAAGGAGAGTC
1283	GGGGAAAATTGAGGCCTTAGCCAT
1284	CTAAGGTCAAAGCGCTGTCGCCAG
1285	GTGAGGCTTACCCCGTGCTCTTGG
1286	CCGTAGCGGTGCTCGACCAGGTTC
1287	TGGGGACGAATCCGAATGTAGTGA
1288	GTCATGTAATTGCATCCCACGGGT
1289	CTTTGCGCGGTGGTCAATAAAAAG
1290	CACTCGAGATTCAATGGGCATGGT
1291	CTCGGGGATGCCCTCTTGGCATT
1292	CGAAACGTGGTGAGAAACCTGAA
1293	GGAGTTCACGAGTCGAGCAGTCGC
1294	AGCCGTTTTCAAAGATCTCGACGA
1295	TGGCTGGACATTGTCTGCAATGCA
1296	ATCGGCTGCCTCAGTCCCTAATT
1297	CCAGCATGGAGTTAAGTGAGCGCG
1298	TTCATATTTACGAATGCCGGGTGC
1299	CGAAATCGCACAGGAATTCGCGTC
1300	GGCAATTTCTGGGACACTCGTTTCA
1301	TTTGTGATTGGGGGTATAACCCGA
1302	CCCAGCTAATCCAGCTTGGGCTGT
1303	AAAATCGTTTGGCTGTAACTCGC
1304	AGGAGATTCATCGACTTCCGGGAA
1305	GCACGGGGTCTCAATGCTTAGGGT
1306	GCGCAACAAGTAGCCTACCGAGGC
1307	TAGCAGGCTGATGCCGTCTACACA
1308	GCAAGCGGCGATCGTACAACCTTGT
1309	GCACCTCTGGTAAGCCTGAAAGGG
1310	CGAGGGCGGTGAGTGCATACCGTG
1311	GGATTAACCGGAACCTGCCCTTCTG
1312	GATATTGGGTCCGGCGCGCATTAC
1313	GGCCTTTAATCTCCGGTCGCAATG
1314	AACCTTAGTGCGGCTAGGTGGGGT

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1315	CACGCTGACGCCAGTGTGGTGAGG
1316	GGTTCCTTGACCCACCGAATTGA
1317	TTCTGACAACATCGACCCTGGCTC
1318	GCGAGCGAAGATAATCCCCAACT
1319	GTACTCTGTGCAACGGTCCCGAGT
1320	ACACGCCAGGAACAGTGTCTGTGA
1321	AAGGGAATTTAGCGCGCTGACTT
1322	TGACGTACGCGTTTTAAGTGGGGA
1323	CTTAGAGGGACGAGGCCATGAATG
1324	GGACGACTCCGCAAAAAGGTCGT
1325	TCAATCCCAACATCCAAAGCCTCA
1326	GCACTGGTCTACCAAGCTTGTCCC
1327	ACTTGTCGGAACGAGACCGAGCA
1328	TCAGGAAAGGCCTAAAGGCGAAAG
1329	GGAATGTAGTCAAGGAGGACGGGG
1330	GCACGTGGTAAATGAATTGGCGAG
1331	GATCATCAGGGGTTATGCGTCGCG
1332	CTCACTATTCTGATTGCCCCGCG
1333	GGGGTGATCTCTCGAACGTCACCC
1334	AAGGTTGCTGCTAGCGTACCTCGA
1335	TATAGATCGCCCAACAGGCAGGAG
1336	GTTTGGACCTGTTGGGAGTGGGCA
1337	ATTGGGGAAAACCCGGTCTCAAGG
1338	TCGACGATAAAGTGCTCACGGGAC
1339	CGATAGAATTCAATGCAGGGCGGA
1340	CGGTTGCTACGGCGGCTGGTTTC
1341	CCAGGTTTCGGTTAGTCGCGCTAG
1342	ACGACCTTACACTCGGATCCGACG
1343	TCGCGTTAAATGGACCAAGGGGCC
1344	CCAGAAAGAAAATGGCGCCCGGAT
1345	GATACATCGCCGCCTGCTAGGCAC
1346	GAGATCACACTCGGAAACCGGATG
1347	ACTTCGCGGAAAAAGGCTGGCATT
1348	CCGAGCTGCACGAGCACACAAAGT
1349	TTCCACAAGGCGGCATAGTGAGGC
1350	AGCAAACCTGGAATCCGGAAAAACC
1351	CGCTATGTCGAGCATGCATTTAC
1352	AGTCACGCCCAACGTCGGTTCTTT
1353	AGTGGGCGCACTTGGCCTTAAATA
1354	ACTTGCAACTTCGGCCGTTTGACT
1355	CAAACATCAGGTTTCATGCCGTACG
1356	AGCGTGACCACCCTACAATGGCAA



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1357	GCAGGCATCCGGCAGAGATGTCTC
1358	GAGCGGCTAAGAGGCCAGACCAA
1359	CACAGAACAGGGTGTTTCCCGCTA
1360	ACTTGCAGAAGGCCCAACACAAG
1361	CCTTCCTGGTACTTTGTGGGCGAC
1362	CTACATGCTCACCCACCAGAGTG
1363	ATTTTCAGAATAGCCCCGCTCGA
1364	CAATTGCTACGTTGACGCCCTCTG
1365	CTGTCGCCTAATCCTCGGTGGCCG
1366	TTTGTGTTGGCTCCGTACATTGGA
1367	ACGTGACGGGAAGGTGGTTGAATC
1368	AGTTCTTGCGTTGCACGAAACAGA
1369	GCTCGCCGCGCGTCTTTATGTCTG
1370	ATGAACATCGCGAGGCAAGCCTTT
1371	CAACCGCGCCACCAACATTAAGG
1372	TGATCGAGGACGGCTTGGTAGCCT
1373	GGAGGCATGCCTTCCGAGAGCAAC
1374	CACCGATCCTCAACGCAATTGCTA
1375	GGCCATGAATTGGGAAATCCATGT
1376	CTGTTCCAGGCGTAACCAGCGGGC
1377	TATGTCTGGCTCGCCATCAGAAGA
1378	GGAGTGACCAGCACAAGCATCGAG
1379	TCGGACTGGAAGTAACTCGCATGA
1380	GTAGGGTCAAGCACGATTGAAGCC
1381	CACCGCGGTTTCTGACTAACGTGAC
1382	GAATGACGCGCAGTGCATTTGAAC
1383	GTGCTCGTCTAACCGCGGATAGAG
1384	GCGGACCTGGGTAAATTGACGCGC
1385	TTTTTGATGTTGCGCACCGGGCTA
1386	TTGCGTCAGCGCATCTGCTCGATT
1387	ATGAGCACGCCAGTTCGTTCCCTTT
1388	TCAACGGTAAAGAATCGCCCCGCA
1389	CGCGATTGACTGAACCACACCTCT
1390	GCGTGAAAGATGACGGCCGGTATA
1391	CATGATTCCACCTCGATCGGCTAG
1392	CTACGACAAAGCAACCGTGCAAAA
1393	ATGCCGTGTTTATCTTGATGGTCC
1394	TTCGTGGAGGGACTTTGGAGATCC
1395	GAAGCGCCGTAACGTACACCGTCG
1396	AGCGTGCGCTTGGCTATAAGGCTA
1397	ACAGTCAGGAGTAACGCCGCTCAA
1398	TTTAGCCGCTGCGACTGTAGGAAA

1399	ACTGTGTCGCAATCAACCCGCAA
1400	TGCAGCCAATGCGGAAGTTAGAGG
1401	CCCGCTATCCCGGTCTTGCAATT
1402	GAGGGCGCAACATATGCAGTGCTG
1403	CGTACGGACATCGATGACGCAACG
1404	AGTCTCCCGAGAAACGCATAAGGC
1405	AGGAAGTGGATGAACGCGGCTGCA
1406	GGGTTGCTCACCCTCGTCATCAGG
1407	TAGGAATGCGAGTTCCGGCGGTAA
1408	CTCCTCACTTCCAAGCTGCGGATA
1409	TCAATAGCACCTAGCATGCTCCCG
1410	TGATTCTGCGCTTTCACAGGTCG
1411	GTATGTGCGGGATGGAAATCACGC
1412	TACGGCAACTGTCGATACGAGGGC
1413	GGTTCCTATCCAGCACTCCTCGC
1414	ATAAGCGCGCCACAGGTATGTACC
1415	GAAAGTCGCCAACAGACTCGAGCA
1416	CGCTAATGCCTCATAGGCGTGTGC
1417	ATCCCCGCCGCACGAAGTACCAAG
1418	GACGCTGCTGATGGCTTTATCGAT
1419	CTCTCCCCGTCGCTTCAGAGATTA
1420	TCATGTGGGCCGTCGTATCAGTTT
1421	GGCCTGAAGGTGAATGGTTACGTG
1422	AGCCTCCAAAGCCGGTAGAGTTCC
1423	TTGTCGTAGGCGCTCACCTTAGGA
1424	GCCTGAGTCCGGGTCGGGAAAGAA
1425	GGCACTATACCGGTTCTGGACGCG
1426	CCGTGTATACGAAAGGTACGCCA
1427	CCCAAGGCAAGTGTGCATCAGTCC
1428	GGAGTGCATCATGGCCAAATCTGG
1429	CCATGTTACGTCTGCGCACCACAG
1430	GGCGTTGAGCTTAAAGCAGCGAC
1431	TTGGCACTCTGCAAGATACGTGGG
1432	GATCTGCACTGCAAGGTCTTGGGG
1433	CGATCAACTTGC GGCCATTCTGC
1434	CGGCTGGGGTCACAGAAACGAGTA
1435	GCGGCTAGTTGTACCTAGCGGCTG
1436	TCGTCACTGTTAGAGAGGCCTCCG
1437	AGTGTCTGTAGCCCTAGCGGCGCT
1438	AGGACGCAGGGATTCAAGTGCAAC
1439	ACCGATGCGCGGTCTGGTCTCATAC
1440	GGCAGAGGGTTAGGGGGTTTTTTT

1441	GGCAAAGGGTGTTTATGGGAGACC
1442	ACAAGGCTTCGGCTGGCAGAATAC
1443	CATATCCGTTCCCTATCGCCAGACG
1444	AAGCCTTTGTGGCCAAGGCCGCGT
1445	CCGAACCATGGCTTTATCCAGTGT
1446	GTTCAGCAGTAGCTCCCTCCTCGA
1447	GCGCAGTGACACCATGATGCTTTC
1448	ACGATCCATTTTGCCAGCATGCAA
1449	TCCCTTCATTTGCGGTTTTTAGCC
1450	TCTTCTTGCCACATTCCCTTTTG
1451	TGCCTTTTGATTGGTGGTCACGGT
1452	GACCCTCACGGTCATCAGAGGGAG
1453	CCGTTCAACACAGTGATACACGCG
1454	CACCAGGGGATAGGTGCGGTACGC
1455	GGTCGGAAGTATCTGTGCGATCC
1456	TGCTCCTTCCTAGGGTCATCCGTG
1457	GTGGACTTTGACGCCGGCTACCGC
1458	CTGATCTGTCGGCGGTTACTTGCC
1459	AGAGGAGCGGAAAAAACCGGACGA
1460	GCGACGAAGAGATCCAGCAAGCTC
1461	GGGACTTCCAGCTGAGGGACGAAA
1462	GGCGCACTCCAATACCCACTGTTT
1463	GCGCTTGGAGACTGTCAGGACGTG
1464	CAAACCGCTGGTTTCTCCACCTGT
1465	GCGATTGCTTGGGATCGGTGACTA
1466	CTCAGCGACATTTTCTGGTGGCG
1467	CAGCGGCGTCGTTTACTCAGGACT
1468	GACAGCCGTGAACGCTCAGCCGTT
1469	GGGCCGTAGAGGCATCGGGTAAAG
1470	CGCCGCTCACCTGCTTAAAGCATT
1471	TGCCAAATCGCAACTCTTGAGACA
1472	CCCCGATCGGGTGTAATTCTCCCT
1473	CAAGGTCCAGGTGACGCAACCACT
1474	CGAGCCTTCAGTGGTATGCATGCG
1475	CAGCAGCGTGCCCATCTCGACTTA
1476	CGGACCAAGATGGCAGTAATCCAG
1477	CTACCACGCTCTGCGCGGGCTGTA
1478	ACGTGGTTAGGCATGAGCTGCGTC
1479	CGACATATCCGACATGACCGGATG
1480	GCGCCCAGGCTGTGTTAGAAAATA
1481	AGCTGGGACTCCGGACCTTGAGTG
1482	CGGTCGTAACCGCTGCTACAACCTT

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1483	TCGTTCTCTGGAACAATTCAGCA
1484	CGGCATCTCCGGACAAAGGTTAAC
1485	TATCTTGTGAGCGCCACTCGGAG
1486	TGCAAGGGAGAAAGCCCCATGAGC
1487	ACTGCATAGCCCAGATCCGCTTGC
1488	TGTGATTCAGTCGAAGCAAGGCCG
1489	CATCCATCTACAATTCGGGCCAGT
1490	ATGAGCCGTTTCAAGGCCAAAGA
1491	AACTGGAATTGCTAGACCCCGCG
1492	CTGAGCTGCGTGGGACAACTCCGC
1493	CAGCTACTAGGGCGCGATGTACCC
1494	ATAATGATGGGACGAGAAGGCCCC
1495	CGACCGAGTGTTACGACATGGTGC
1496	TGCAGTACCCGCCGCTCCACTAGT
1497	ATGCTAGCGCGCCTGTCAACGTAC
1498	AGACTCACTGCCGGCTGATCAAAT
1499	GCCTGGTGCGAAGATAGGGATTCC
1500	GGAAAGTTGGCGGATCCGAGCACT
1501	GGCAGTGAGCAATGTGTGACGAGG
1502	TGAGGTCTCCCGGCGGACTACGA
1503	CTCGCCTTAGATCGTGGTTCCGCA
1504	GTCGAGGAATATCATCGCAGCCAG
1505	GCGAATGCAACGAGACAAGAAGGA
1506	TTCGCCACCAAGTCGGCATTGT
1507	CGGTGGCTGACACTTGCCGGATTG
1508	CAAGGAGCAATCAGATGGTCGGAG
1509	GTGACCCGGTCCGTTCTAGCTGTG
1510	CTCTCGCCACATAACTGCACAAA
1511	AAACCTGCCTAAGCAAGCACTGGA
1512	TTCCATATTGTACCCCGCGCATGC
1513	TGCTTGCGATATCACGATACTGCG
1514	TTAGTGTTGAGCCTTGAGCCGGC
1515	CTTGTGCGCGAGTCCGTCTGGGA
1516	GTCAGCTGCCTGCTGGTGCTCTTC
1517	CATCCCTCGAGGTGTAGGCAACAC
1518	CAGATGCACTCCGACGGGATTGAG
1519	CTGAGCCTCGCGAAGCTGTGGCAT
1520	GCTATGCCACGCCGAGATAGAGC
1521	AACACCAACCATACCGTCCGTTCA
1522	GCCCAGAGCTAAAGCATGTCTGGG
1523	AATGCTGCAATGCTAGCGTCGCTA
1524	TCCGGACGCAGTATCCAATCCGGA

1525	TAAGACCATGTGGCACCAAGGTGC
1526	ACAGCCACACACACGCGCCCACTA
1527	TAGAACCGAGCACGGCGCCTTGTA
1528	TTCCAGTAAGCTGGCAGGACCACT
1529	CTTTCGCAGGTTCGCAGACAATCC
1530	TACGTCCTGTGCTGTTGACACCGG
1531	GTTCCGGTCAATGTTTCGGGGAGA
1532	CCCTGTTGTGAAGGGGTTTGTGA
1533	GGCAGATTGGTGAACCCCAGATAA
1534	CCCTCGGTGTGTTCAAGCCAAATC
1535	CCCGCGAACATTTGAACAGCTTAA
1536	CCGTGTCAGTTGCTCCCTGGCAGC
1537	TCCGTCTCAGCCGCCTCCCTATCC
1538	ATAGCTGGGTCACCACAGGCGGTC
1539	ATAGGCAAGCGGTGTAGCACAGCG
1540	TTAGAAGCCGGTCTGGATTTGCGT
1541	TGCCGACCTTTACCAGGATCCTCG
1542	GCCCACACTATAACCAAGCTGGCA
1543	TTGCGCCACTAGTACGGATCTCAA
1544	CTTGCAAGTTTATGCTGACCCGTCC
1545	TGCCTCCAAATTACTTACCGCCGT
1546	CCCGTATGCGGAAGCTATGGGCTA
1547	TCGTTCAACCCACACTTCAGTTG
1548	CAATGTGGGGGACATTTCAAGTT
1549	TAGCGTCGCACAAATGGCTGACCG
1550	GGTGGCTTCGTGACAATATCGGCC
1551	CAGCGGCGTCCGAAATTGGCTCTC
1552	GGCTTGCTCTCGTTTTTGATTGCA
1553	ATGCGAGGAGGACACGACCGTTCC
1554	CCTGTTCACCTACGACCCACGGGAA
1555	GTGCCACGGAGTGCGACTGTTGCT
1556	ACACATCCAAGTCTGACGATGGCC
1557	CAGCCCGAAAGGAAAGCCTCCGTG
1558	AACTGAATGTAGGTGGGCCCTGT
1559	ATTTTCGACGATAAGCTGGCCGGT
1560	TGAGGGAGAACCCGAAATCTGCTT
1561	GGCGACTACATCCCCAATTGCTTG
1562	GCAGACGCGGCCTTCATACTTTT
1563	ACAACCACATGACGTGTAGCTGCA
1564	CTGCTGGGCGCGCAAAGCTTGTTG
1565	AAGCCTTCTTTGGCTTGCTCCGCT
1566	TACCTGCTGCCTGGAGCAAGGCAT

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1567	GACGCCGCAGCCATGAGTGAGTGT
1568	AGTTGGCCGCTTATTTTGCTCACC
1569	AGGCGCACGGAGAACATTTGCCAA
1570	CCAGGCGCCTTCGACAGATCCTCA
1571	GTGTCCCCTCCAGCTAGCCAGTTT
1572	GACAACAAGCCAAGGTGACACGTC
1573	CTACACCGCTCGTGACTCGGCAAA
1574	TGGTGCCATCAAAGCACGTTGTAC
1575	ACAATGCGTGTTGCGAAACGCATA
1576	TTGTCCAGCCATTGTATTTTGCGC
1577	ACGAGAGATAGCGGACTCCTCCGA
1578	AGCTTTGTCGTCAGGCGAGCTCTT
1579	GACAGTCGGCGTGCAGTTTGTGT
1580	AGCTAGCGACGGCCAACTCACGTA
1581	CTCCTGTTGCGGGCCGTTACTGGT
1582	ACTGACCGACGCAGTGCCACATAG
1583	AGGTAGGGTCTGGTTTGAATCGCA
1584	CCTCCATTTTAGCGCGTTGCCAAT
1585	TTCTTAGGATCCGCGCACTCTTGG
1586	GTGGAAGGTGTCTACCGTGCGCAG
1587	GTCACGCGCGGCCAATCACTCG
1588	TCTCGGTCACCCGTCTTGACCCTT
1589	GCCCTCGACGAACTCATCCTGAAC
1590	TCCGGCGTACTCTGACACGGCGAT
1591	AGCCAAATGCTTTCGTGGTTCGGA
1592	ACTCCACGCCGCATGTTGCTGTGA
1593	GCTTCGAGTCGGTGGCATCTGTAT
1594	GGTCTTGGGCCATCGACTTGCTGC
1595	GGTATCGGACTGCACTAAGGGCAA
1596	AGCCCATGCGTTCGGATGATTTG
1597	GCCAGGGTTAAAAGTGATGGGCTC
1598	GACGACGTGCTGGCTACGAAGGGG
1599	TCCTATTGACCGTGATCGTGATC
1600	ACCCGCCTCGACTCCACAATAAA
1601	GATGTGGATCACGACCTGCCAGTA
1602	GTGCCATTGCCACCCATAATGCGT
1603	TTAGCCTGTGCACCCAGTCAGGAG
1604	TCCGATGGGAGAGGCTGATCTCAC
1605	CACTACTGAAGTGGCCTGGCGCTG
1606	TGCGGCCATAGCGATGTGATAGAT
1607	GATTGCGCTTAACGGAGATGCACG
1608	TCACGTTTGACAACGCCAAGCATT

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1609	GCATTGTTTGCTAAAGGCGGCATT
1610	AGTCGCTCTACGCGTGCAACGCTG
1611	TAGCTCCATGGAGGTCCGAAAGGG
1612	GACCGGTTGGACCTCACTGGCTTC
1613	AAGCCGGACAGTCAATGTGCGTAT
1614	TGCCTCGCTGAGTTCTTCACCGTG
1615	TCGTAGACCTTGCTTTTGGGCTCA
1616	ACCGCTATGCGCCCTACAAAGCAT
1617	TAGCGTCACCGTAGCTTGGGGCAG
1618	CTCTCAGCAACTGATGGCACCGGA
1619	AAAGGAAATGTGGTGCTGGTCGGC
1620	CCGGCTTAGATGGAGAACAAGTGC
1621	AAGTAAATCGCCTCGCCCAAACCG
1622	TGGGCTGTTGAGCCTACCGGACGT
1623	GTTTCGGTTCAGCCATGGGCCTAC
1624	GGCCAACATTTCTAGGGGAGTGCC
1625	TTCTTCGTTGGGATTGTCCTCACC
1626	TGCACATTGGGGTACGGATCTGAC
1627	GGCAGTTAGACGGCAAACCTGCAGG
1628	CGCGTCAGGCTATGAATGGCTCTT
1629	GCTGAATGCAAACCTCGGAGCCAT
1630	CGCTCTGGCGGATTGATTGTTTC
1631	TTTTCAATCAACCCTCCGGACGTA
1632	GTGGTGGAGTCTGAAGCACGACAG
1633	AAACAGGTCCGGATGATGTCTGGA
1634	GTACCGCGTGTACGCCACCGTTAG
1635	TCCAACCTACATTTGCGGAAGGAA
1636	GACGTACCGTCGTCCCGTGAGTTG
1637	GGCAATCCTACAACCGACGCTGAT
1638	GGCGGCTGCAGGGTCTACATCGAG
1639	ATACTACGCTGCAGCTGCGCGGGC
1640	GGATCGCAATCCCTCCGATGACGA
1641	TGGCCTTGACGCGGAGCCGAATCT
1642	AGGTGCCGACGAAACGACGAATAT
1643	GCTGTTTCACCGTCGTCGTTGTTG
1644	CGGTCCCAATGTTACAACCCAGAC
1645	GCAATTCCAGCCACTTTTGACCAA
1646	ACGGGCGAAAGCTCGGTACGGATA
1647	CGACCCGACTTTTGCTTTCGAGTG
1648	AATTCAGTGTTCGCGTCATGGTCG
1649	CCTGTATGAGGTTCTGGGTGCGCT
1650	TGGCATACTTGGTGCAAACGCCGT

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1651	TCGCCAGTACAGAAACATGCGGGC
1652	CCCGCTGTTGCTCTCATCGTGGAG
1653	GCCACAATCTGACCCTGGGAATCA
1654	GCTCAGTCTCGGAAGTTTCGGCTA
1655	CTTCACGGGCCAACGACGGTCGAG
1656	CGACAGTTCGGTCCGTCTTGAGGA
1657	ACGGAGACGCAGTCGAAACGTCCC
1658	CATGCATCCGATTAAGGGGATCAC
1659	ATTGCGGGAGTCCCTAGCTTTCTG
1660	GTGTGGAAGATGCAATTGGAACGG
1661	ATACAACGGTAGGTGACAGGGGCG
1662	GCCGTGGGAGTAAGGGTACAAAGG
1663	GCACGTAGGTCGGCTACTACTCGG
1664	ACTGTGATCTCTTGGGCAAAGGGC
1665	CATGCCTGAACAATCTCGCATCCC
1666	GAGCCTGGCTCCACAGCTGTGCTC
1667	CTTTCGATACCATCGTTGGCGATC
1668	CCCGGAGGTGAGGCATTGAATATG
1669	CTCATTGAGCTAAAAGCGGCTGGA
1670	GAAATGCCCTGGGGACTTTTTGCC
1671	TTTGCCTTCACAACAGACGCAGCA
1672	AAATCCCAAGACGTCGGGGCGTAT
1673	CAACGGGCGGTAGCTAAACCGTAA
1674	GGCCAACGACAATGCGAAACCTTC
1675	GACATCACGCAAAATCTCAGCGCA
1676	ACGTTCCGTCCACAACCGTATGTT
1677	GCTCATAGGTCTTCCGTAGCCCGT
1678	GAAACGAGTCTCTCGCGCCCTAGA
1679	CGGGACAGAAGCAAGTTACATCGG
1680	TGACCGCTCGATACCAGGAGGGTG
1681	CTGGCAATAAAGACCTTCCGACCA
1682	TGCGCGACGTCATGTTGGTGATTA
1683	GTTGGTTGTGGGAACACACCCGCT
1684	TGTGGGTTCGGAAACACAGGAAGT
1685	GGAAAAACGGCAATTAGCCGAGT
1686	TGGTGCGGAGTGCCCTCTATTGGG
1687	AACCAACAGGCTGCAGCCCAGACT
1688	AAACAGATCCATCTGCACGCCAGG
1689	GGAATACCGCGGCGATTATGGCTT
1690	TACTGTTGCGGGCAAACCGTCACT
1691	GATCTCTCGTGGAGCACGTTTTCC
1692	GGCATAGCAAACCTTGACCTCCAA



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1693	ATCTGGGATTCGCGAGCCAATATC
1694	CGATCAGGATATCATTTACGCCCG
1695	ACGGTACCGAAACGGTCTCAGCGT
1696	CTCCCATACCTGCGTTCTTACCGA
1697	GCACGAGAACCTAATTGTCGCACA
1698	GCCACACGATCAAGACAGCGCATG
1699	CCCGTTAACTCACGAGCGGTCAAT
1700	AGAGAAGGTCATTGCCTGTCGGTG
1701	CGGGCCCTCTTAAAGTAGAGCAGG
1702	ACATCGCGTCCGAGGGAGTTAGCG
1703	AATGCCTAATCGAGCCAGCGGATC
1704	CTCGATCTTTTTAAACCGGCGCTT
1705	CGTTCCTGGAAGGCAGGGTCTCAC
1706	CCTGTGCTTACTATCGGCGATCCA
1707	GTTAGTCGCCCTATTGGCCTGGTT
1708	CCGGTGAGATGACTGTAAATGCCA
1709	CGTGGTTTAAACATCGCGCTTCG
1710	TAAGACGCAGAAGATGGGGTCCAC
1711	CACCACAGCTTCTTTGTTGACCC
1712	TCGGGTCCGTACCACCACTTTTGC
1713	CCAAGCCCCGAGTACCGAAGATTT
1714	TCCGTGATATGGTCGTGGCGCGGT
1715	TGTCTGTGTCATGGCACCTCGCAT
1716	AGGACTGCACTGTGCACGTCTGAT
1717	CCATCCTCATGTACAGCGCCGCTG
1718	GTACCCGCGCCTTCCTCGACACAG
1719	ACGGGTCCTGGTCGACTAAGGCTT
1720	CGTATCGAAGGCGTGTACAACCGG
1721	TGCCCGCCCTTTATGCAACGCTCA
1722	AAACTTACGAGACGGCGGCTGCCA
1723	AAGTCTGACAAACGGAACGGGTGT
1724	TAAGCGCAGACCAAAGTATGCGGC
1725	GCAGTTTTTCAGATCCTCCGCAA
1726	TCGGAAGCATTTACGCGATCTCAG
1727	CACAGAAACGGTTGAACGAACGCC
1728	GCATGCTCAGATGGTCGTGCTCAC
1729	AAGGATTCTCGCTTCCGGCATGAT
1730	GGTGGGGTAGCGCTGGTATGAAAA
1731	ATTATTACGGGACCGAACCAACGG
1732	GCGCGAGTGTCATGATGTTACGT
1733	GACATTCGTGACTTGGTCGTCCGC
1734	TCATTAGTGCAGGCACCGATCAAG

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1735	GAGTTGTGCGGAGTCATCGGAGTC
1736	GCCTTTACAGATTTGGCGGGCTAT
1737	ATGGCGTTTGCGAAGTCGATACAG
1738	TGCATCGGCCTCAATCAGAGAACT
1739	ACAATCATGGCAATCTGGCAAATG
1740	GACGTGGAAGAGTGCAGATCAGCA
1741	AGGGCAGGGGACGGACAGTAAGTC
1742	GCATAGGGCGAATCTAGTACGGGC
1743	TCCGGCGCATCCTCATTAGCAACT
1744	TGGCCGCTTCCACTAATATTGGAC
1745	CCGGCGGACGGCTCTTGTCAATGA
1746	CGAGCAACCCAAAAGGAAGCAGTA
1747	GCGTATGATTGCGCAATCCGCCAG
1748	AGTACCGCTACAACGCTGGTTCGC
1749	GGGCAGGCCAGGTCCACCTGAGAA
1750	CCACTTCTGTGACCGAACCGTGCT
1751	CCTGGTACCAGGCAGCAGTTGATT
1752	TTAGGGTACCGTCGAGAGACGCCA
1753	GGTTGCTTGTGCGCGTGAGGTAGT
1754	TGCTTCGACCGATGAAACTCGAAG
1755	TGCCACCCATACTATGCCCAGTGG
1756	TGTGCGGCAACGCGTGAAGACGTT
1757	TGAGAGAAGCTGGCCTCGGATCAG
1758	TATTGCGAATTCGAGTACGTGCCC
1759	CGAGAGGGGTTCGCCAGTGATCGA
1760	TGCCTGGGGTGTCGTTCTAATTCT
1761	GTGCGTCATTGTGGGTCATCCCAA
1762	AGGGCTCCCAGCATACCAACGTTG
1763	AACTAGCCGCACCTTTGTGCAGAG
1764	TTAGCCCAGCCCTTCAATGGGAAC
1765	CGGCCTCGGTTGTACGGGTAGTCT
1766	TCTTTGAGGCGCGGACCCGCATAT
1767	GATGGTTCGCCCTTGTGTGCGAGC
1768	GAGATTCAATACAGGCCGCGGGTC
1769	AGGGCGAAGGAAGGTTCCGTTTTT
1770	CTCGACCCCTGCCACTACTGGTTC
1771	TGTTCCGCGGTCTACGCATTACTG
1772	GAGACGACGTCCTACACCCGCTAA
1773	AGATTGCGACAGCGACACGTGATT
1774	GATACCGTTGGGCATTTCTCGGTA
1775	GATTGGGAGGCATTGAGCGACGGA
1776	AGGAGGAAACGAGGGCGTAGGTTC

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1777	GCCAAACAACGTCTGACGCCTAGC
1778	TTTAATGCGGAAAGGATGCACGCG
1779	TTATCGGCCGTTAAAATGGGATGG
1780	CCTTGATTGTTTCATCGCTAGCA
1781	AAGTGAACGTGCAGTGGTCTTCGA
1782	TCCTTACCCCTCGTTCAAACGCCT
1783	ATTCCTGAACCATGCATGGCCTGT
1784	AGCGAGACGCTCGATCACGAACTA
1785	GCTGGTCTGGCTCGCTGTTTAGAA
1786	CGTGCGCGGCATAAAGATAGGTCT
1787	TCTGGCACTCACATCGGACAGTCT
1788	ACCATTGGAGGACCACAGAGCTCC
1789	TCCAGGGTCGGAGTACATGGCGGG
1790	ATATGCCGTCGGATCGTACACGCA
1791	TGCTGGCGTCAACACTTCCCGATT
1792	CAGGGCGGTGCGGTGAACTAGCCA
1793	CATGGACTGCCGTACATCAGCTGG
1794	CCGGCCATACGCTGGCAAGATTAC
1795	AGCGGACACCTGTACTCTCCTCCA
1796	GGAGCCACACCAAGTGAAGATGGT
1797	CGCCACCGGAAATTGAAAAGACTG
1798	TGAAACGGATGTTGCTTCTTGACG
1799	TTGAAGCGGTGAAGAGCCTGTCCT
1800	CGAACCAAGCTGCATTGTCAGTGG
1801	GAGTCTGCGCTTGCAATCTTTGCG
1802	GCTGGGTATAGTTGCCTGGCAATG
1803	GCAGGCGTTCCATATTGCAACCC
1804	GCGCCAATAATACCTCCACCGCG
1805	TGGCGTTCAGTGCAACGCTGGTTA
1806	CAAACTGACGGGTATGGGAGCGC
1807	AGGTGTCGCTGGAACCCGACTTGT
1808	CTTCCAAAAGCGCAATTGGCTTTG
1809	TCGGGCTTCTCGCAATTCTGTCAG
1810	GCCAAAAGAATGCGCTGGGTAGGT
1811	TGGTGCCCGCACCGAGAGACTGTA
1812	CGAGGCCGTAGTGGGGACTGCTCT
1813	CGATCTGCGCATAGAGGGGACTTT
1814	TGTGCAATCGGCCTTCTCAGAGCC
1815	GATCACCTGGACCGCTACCGTTTT
1816	ATGGGGAGTTAAGGACCCTGCACC
1817	CATTGTGGACAGCCAATGGTGGCT
1818	CCATCACCATGCCACGGTAAGATC

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1819	GCACCCGTGTCGTTGGTTAGCAAG
1820	GGAGTGGGTTCCGCGAATTCAGT
1821	GGGGATTTCTTTTCGCAGGCTCGA
1822	CATTGATCATGTGCACTTGACCA
1823	AGCAGCGCTGCGCTTGTTTCGGAT
1824	CGAGTAACGCGGTTGCTTTGCGAA
1825	TGGCCTGGAACATAGGTGGAATC
1826	CGCACACCAAGCGTTTATTGAGAA
1827	TCACCTTCACAGTGGGCATACAGC
1828	CAAATATCCCTGAGCCCTCGAGCT
1829	GGGAGCTGGTGAGCAGATGTAACG
1830	AGGATTGCTTTTGCGTTATGCGGA
1831	ATCGTTTGGGCGCTACGCAATTGT
1832	CCGATTTGTCCCAAATGCAACGTT
1833	AAGGGTCAAGCTCATGGAGCGGAA
1834	TCTGACGTCGTTCAAGGGCTCGCT
1835	CGCACCACTCCGAGGTATTTGTCT
1836	AAGGGGTGAAAAAGGAGAAGCCGA
1837	AAACCACGCAAATGGCGATACCAT
1838	CAGAAGGGATGACGCCTTAAGTCG
1839	CATGACGAGAGCGGACCTGAAGTG
1840	CTGGACATGTTTGTTTCGCCACTG
1841	AAGACCGACTCTCGTCGTTTGCAC
1842	GCGCGATTACATACCGTTTCCGTA
1843	CACTGACCGGACCCAACCTAACAT
1844	AGTGCAAGTCTAGACACGCCCCGAG
1845	GGTTGGTGCGAGATCCTGGACTGT
1846	GGTCGTCCCGAAACGTAAACGAGG
1847	GACTAGTACGATCACGGGGCGGGT
1848	CCGACCTGACCCTGTGTACAGGTT
1849	TGCTCACTGCCCACACTGTTATGG
1850	CGAGGAAACACATTTCTTCGGGCC
1851	TGGCACCGGGTGGATTCTTGTCTA
1852	GAGGCACGGTGATAGTGGTTGTGC
1853	ATGCAGATGGATCTTTTTCGACGC
1854	TGCGATAGCCAAAGAGTCGAGGAC
1855	ATGGCGTGTACGCGAACTGCCTGG
1856	CAATGCAGCTCGGAAGTCAGGTCTG
1857	AGGATCAGTGACATGTCCCCTCA
1858	CACATCTTGGCTGTCACCCGAGAA
1859	CGCATTATCACCTCAATGCCAGTG
1860	ACATCCGCAGACTCCCTATAGCCC

1861	GTGAACCCGAACGAGGGGAGTCTC
1862	GCGTAGGGAATTTGCCTCACGACT
1863	TTTACGCGTCGCTCGGTTGTAGTG
1864	GAGAGGCGTCTAGGCGGTTCTAGC
1865	GCATGCTGATAACGAATGCTTCCC
1866	CTGAAGCTCGTGTGCGATGAGGGA
1867	ACAACGGCATGAGGAGGCTTTTTTC
1868	TTTGGAGACGCCAGTACGCGTGGT
1869	GCTATCATTTGGTGTAAAGCCCGCC
1870	TCAACATCCAGGGCGGTGCTTGGT
1871	TTCGATGTAATCCCCAAAGATGCC
1872	GGACCTTCGGCAGGTTATCGCCGT
1873	AGTAAGAAGAGGCAGGCCCCACCT
1874	AACGGCTCCCCGTCGTA CTGCTTA
1875	CCTATACGTCGTTGTTCCACGTT
1876	CCGCGCAGGCGCTAATACTCAAGG
1877	AAATGGGCCAGTGAAATCCTTGGT
1878	ACGGTTTTCGAATACTGCTGGGCAG
1879	CCGCTTGAGGTTCAAGTCAGAGCT
1880	ATCGTGCCCGAAGACACTTAAACG
1881	ACCTGAACCAGGGCGATTGCTTTA
1882	ACCCTATACGCTGGGCTAAGCGGG
1883	TGTTTCGCGACTAGAAGCCTTTGC
1884	GAAGTTGGCGGCTCACCCGTATTA
1885	TGGCTACACCGCTTAGGAGGAACC
1886	CCACAGTTGCGTGACTTACATCGC
1887	ACTGCCACTGCGTCTGAAGAGTGG
1888	GCGCCAGCAAATTTCTGTGTTGT
1889	TGCCTCCGTCGAGCCGAATAGCCA
1890	GTACAAACGGGCGCTATTTCTGTC
1891	GCTTCCCTGGCTCTGAACGGAAAC
1892	CGGCTACCCAGGCAGATAAGCTGA
1893	GGTTGGACCCGACAGGGAATTTCC
1894	GGGGAATACCCGGCGTTTGTAAATA
1895	TGGTTCGGTGAGGTTATGTTCCGT
1896	TCGGTAGGGTTCACTCGCTGAGGA
1897	TTCCGAGTGTGCCGGTGCTAGTAC
1898	TCGTA CTGGAATGATGGCCGGGCC
1899	TCCGTCGACCGTCCAGCGAAGTTT
1900	AGGGAATATAACAACACCGCGCAC
1901	ATGTCCCGGAAACCAGCTACCTCA
1902	ACCAGCGACTTAGATAGCCGTCCG

1903	GGAAAACCTCCTTTGCGTCAACCA
1904	ACGTGCGTGCATACCCAAGAGGAC
1905	ACGCCACTTTCCCTAGAACCAACG
1906	CGAAGTACGCAATAGTGCCACCCT
1907	GATCCCGGCGGATCACCTATCAAT
1908	AGAAAGCGACCGTTTCAGGCTAGC
1909	CGCTCCCTTTCATAGTCTCTCCG
1910	GTGGGTGGTCATAACGACAGCAGA
1911	CTGGAGGCTGCATCGTTCGTAACA
1912	CACCATGAGTTTCGGAGCGAGGAT
1913	CAAGCTGCGTTCGATGAGAGATTG
1914	CCTGGGAGCAATGACCGCTCTGGT
1915	TCCGGCGCTCTACCAAGATGAGAC
1916	CGACCGCGTCGCGTATACTATCCG
1917	AACATTGCTAGTGGGGTCCAACA
1918	TGTATGATCATCCGACCGAGCAGC
1919	AGTGCGCCGAGAGGGTGAATAGAC
1920	AGGCTTGTTCTGGACCAGCACCAT
1921	GGGGCCACATAAAGAATTCCGAAC
1922	TGGTGAAGATAAATCCGCATGGCA
1923	ATTTCCACCACGCTCTTGCCAAAT
1924	CGCGTAAAGCTGTCACCGATGACC
1925	TCCCAACCGGTAACAACAGCGAC
1926	CCTCTGCTCGCCTTACACCCATGG
1927	CAAGCTGCTCCTGTGCTGAAGGGC
1928	AAACGAACGATGGTCGGTAGACCG
1929	TCAGTTCGATGGCTATTGCGCCTC
1930	GGCTCTCAACGGACGCAAATCATA
1931	AGTAGAGTGTTGCGGCTGCCGATC
1932	AGACACTAGACCGCCGTGACCTGA
1933	ACCGAGCACCGAATTTCTTGTC
1934	CCGTGGCCAAGATACGAACGAATT
1935	CCTCCTACAGCATCCACATGAGGG
1936	CACTCGGCAAATACGTATGCGCAT
1937	ACCGAGTTGAAGCACGAATTTGGG
1938	GACCACCTCGGAAGATCGTTCTGC
1939	TCAACTGGGCAAACGAAGAGCACA
1940	GCTTAGCCTCACACGTGCATACCA
1941	CTGCGGTCTCCAAGTACCATTTCG
1942	GTTCCGTATTACGGCGGCCATAAG
1943	ATCGACGCAACCGGATAGTCTCTG
1944	CGCAGATAAACCGGCATCTTTCAG

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1945	ACCTGCCAATACGGGTCTACGGTT
1946	ACACCTGTTGCCATGCTGATCCGT
1947	AAACTGTCTACTGCGCAATTCCGC
1948	GCAACTAGCCCGTGCTAGGATCGT
1949	TCGTAGTGGTGGATTGTTGTGCGT
1950	GGCTTACTCCTCAATTGCGACACG
1951	CACGACTCCCTGCCAGATTTGATT
1952	CTTAGACGTGCGCAATGTCACGTC
1953	CTCAGAGCACAATCTGCCCTGCCT
1954	GCTAGGAAAGTCGGCATTGATGGG
1955	AAAGCCCCAAAATTCCGCCTAACC
1956	GCGCAACGCTAAGGGACTATCAAG
1957	CGTCCGCTGGGATGAGTCTCCTGC
1958	ACAGGCCTCGTGATTGGTGTGGGT
1959	CATTCTCCTCCGGGACCACGCCT
1960	TCGGAGTTGACCAAGCTCAGTGCG
1961	ACGCGCCACTGCAATTGCAAACAC
1962	AGTTCATGGAGCCGGCGTATTGTT
1963	ACGTTTAATGCGGGGCCCGCTAC
1964	TGAGGCTTTAGCCTACGCGCAGGT
1965	CAGCGTTATGAGCGCGGAGTTTAT
1966	GTCCACGTGACCACGGATAGTTGG
1967	GATTATGCTCCTACGCCTGCTCCG
1968	TCGTCAAGGGCATGATGTGTGGGA
1969	GATGGACCGCCAAAGACACCTTGA
1970	TACACGAGGATGGGGTCAAGCTTT
1971	ACACGCACAAAACGTTTGAAAGGC
1972	GTTATCGTGGGCCGATGGTACTGA
1973	ACATGACCGTATCCGCCTGCTTCG
1974	GAAGGCGAACCACTGAAACTACGC
1975	TGACTTTTGCAACGGGTGGAACCA
1976	TGAATTCGTAGGTTTTGGGTGCGG
1977	AGCATTTATGAAGCGGCCATTGCG
1978	TGCTCCTCGCGTTGGTACCGTGAG
1979	CGCAGCAAGAAACAGCAACTGTTG
1980	AGACGCTTGGAGTGAAAACTCGGA
1981	CATTTCGTAGAATGCCCCAAATGGA
1982	CCAGAAGGTTCCGGACCCGTCGTG
1983	GAGAAGCCGGTTCTCAGAGCACAT
1984	TTGCGTTGCAAGATATCTGGCCCG
1985	GGGTTGCATGTTTCAGGCAAGACGA
1986	CTCACGAAGGTGACATATCACGCC

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1987	GCCCGAGATACGGGTTCAAAAAGA
1988	CATCTTCGCGCTTCTTCACTCCGC
1989	TTACACGGTAAGCGTACGGCCGCC
1990	ACCTTCGGACAATGTGGCGTTCGC
1991	TGAATGGTTCTGCTAGGCCACAC
1992	CACGCCTGTCTGACATATGGATGC
1993	CGCCTCAACCCAATCTGAGAACGT
1994	TTACGCTTACTGCGAGCTGGGTCC
1995	GGCTTGTGGGGCAATACGCATCTT
1996	CACTCTCCTTTGGATGCGGAACAA
1997	CTTCGAAGCACTTCAGACTTGGGC
1998	GACCAGCCATCACGTAACGGCCCT
1999	AGGAACCGGATGTGGTTATGGAGC
2000	ATCCATGGGCAACTGAGCCTATGC
2001	GGAACAGCACTTGTTACCGCCAC
2002	TGGCTCGCTTCAAGCCTGTTTGCT
2003	CAAACGTGAGGTCATGACCACCAT
2004	ACCGATGTCTTGAAGTCCGGAGGT
2005	CGAAAATGCATGATGATCTCCCCT
2006	TTTGGTATTCTCGCTGCACCGTTG
2007	GCGTACTCAACCACATTCCCGACC
2008	AGCAAACAACAGCGGTCCGAGCAT
2009	GGACTIONGAGCGGGGATAGCTGAG
2010	CCTTAACGAAAACCTGTCGACCGC
2011	CTCGATCGCATAAGCAAGAAACCG
2012	CCCGTTGTTTGGGCGACAAAAGT
2013	CGGCGGCTCTCGCATGATCTCGTT
2014	CGGATGGAGAGGAGTCTACGTCCC
2015	ACCAAATCAGACTAGCGACTGCGG
2016	CAGAACAATATCGTGCGTCAACCG
2017	CCTTTGCGCGCTCCGAGTAAGGTA
2018	GGAAACGGCACCTATCTGTCGTGA
2019	CGACCGACAAAACCAAATGCCGCC
2020	CCAAGGTGTGGGAGCTGAAGAGA
2021	TTAAGTGCGCATAGTCCTCGTGGG
2022	GCCTGGTGGGGTAAGTCATGATGC
2023	GAGCAGCAGATTGATGCGCTTATG
2024	TGCGCCAACTTCCGGAATATTTGC
2025	AACCCCATCATGAAATGCTCTCCG
2026	GTCCAACGGTACTGGCGTGATGTT
2027	ACTCGGCTGATCGTGAGATGGTGA
2028	ATTCGTGGGCGCATCTCGGAATGT



2029	TCCCGTCCTGTAATCCAGGGAACA
2030	CTTCGCTGCACCTACATTGCGCCA
2031	GCGTGTAGATGACTGTGCTTTGGG
2032	CTATGGTATCGAGACATCGGCGGA
2033	CCTCGTACTCCGTCGTATGCACAA
2034	TGGTGCGTCCGTAGTGCCTGCACT
2035	CGCGATCCTAGTTGAAAGCTTTGC
2036	ACGATCCAGGTGTTGGGCACTAAG
2037	CCAATCTAGGATACACCACGCCCG
2038	GATACGTGGGGTATAGGCGGGCCC
2039	CATGGAACAAACCGTCGTAGGGGA
2040	ACACTCGCGCAGTATTCGAGTCGT
2041	CTCAGTCTCGAAGGTGATCCGACC
2042	TCCCAATCCCCGTGGTATCGTCGT
2043	AATCAACGTAGTTCCGGTGGTCCG
2044	CTTAACAACCCAGGGGTTTGGGCT
2045	CCATCCTGAGAGTGACGGAGGTGC
2046	CTACCGCTGCATGGCGTTAGATTG
2047	TTATTGGTGGCGGACGGAGTGAGT
2048	TTAAGGGTGAACCAACCGCGTGA
2049	TTTGATTGAAACGCTGCGCACTAC
2050	TCATGTGTAGGTGCGGCGCGTCAC
2051	CTCCGAACCTTCTGGGCCTCTTTT
2052	CTGTTGCCCATTTGGCCCGACACTC
2053	CACGATCGCTGAGCAACACATCAC
2054	CGGATCATAAGCGTCCGCCTTCGT
2055	AGGTAAACGCAACATGTGATCCGC
2056	GGGAAAAACAGCTAAGCCTTGCGA
2057	ACTTATTGCCGGGATCCGTACACA
2058	TGCGGTCTGGAAGGAAGGGAGGG
2059	GCTGCCACCTGGACATCGCATACA
2060	GCAGGCATGACAGTGGCGTAGTAC
2061	GCGGCCCTGATGGTTTGGCTGAGC
2062	TCCCCATTTAGTCCCCTCCATCAC
2063	GCAACACAAATGCGAGCGTAGGAG
2064	GGCGTTTGTATTGAGCCACGTAG
2065	GGTAACGTGCGACGTGGAATTCCG
2066	ACTTCACAACGCTCCGTTGGACAC
2067	CCGAATTATAAAGCGCAAGGCACA
2068	GGACCCGATAAGACTCTGACGCCG
2069	ACCCGTTTCTCGTAGGAACCTGCT
2070	CACGTTGACTGTATCTGGTTGCC

2071	CCTCGGATGGGCCCATGACCTTGA
2072	GGACGCCTGCTGTAGGGGTTTGAT
2073	CTCGAGCGTGGGCTAAAAGAGCAT
2074	TTTACTTCTTAGGGCGCGTTTGGG
2075	ACCACCAACATAGCGCGCACTAGT
2076	TGGTTACACGGCAGCCCGCGTAAG
2077	TTATGGTACGTTGCTGCGTGCGGG
2078	ACCGCGGATCTAACGAATCCCATT
2079	CATGATCCCGCCCTTAGGTTAAGC
2080	TACCGCTTCAAAGGGTTGCCGAAT
2081	GCACCGCGTCAATATTACCGAGGA
2082	GTGTCGCGGCTTTACAGAAGGAGA
2083	GCAAGCCATACCGCAATAAACTCG
2084	ATGAGGTCGTGCTGCGTTCACGAG
2085	CGAGACTAGTGCCGATGCAGGGTA
2086	GCCTCATCATAGACGCTGGATGCA
2087	GACAGGCGTCGGTAAGCTCTCAAG
2088	GCTACGAATCTTCCCTGTGCGCCAC
2089	TTTGGCAGAACGTACCAGTGGGGT
2090	GGACAATAAGCACCGGAGAATGCG
2091	TCATGAACCTTCTGATGCCGCGAA
2092	CGCCGCATTACCTTAAAAACGTGC
2093	ACGAGTCCAACCGCCTCATTGATT
2094	GCGAAGAGTTGCTACTCTTCCGCC
2095	CGTCGGCAACAATCTTTTCGTGA
2096	AATCCTGTGCACCCGTGAGACGCG
2097	AACCTATATGCATCAACGCGAGCC
2098	GAACCTGGCAAAACAGCCCGGAAA
2099	CTCTATGGCCGTTTGCCGTCTGCA
2100	AGTGCACCGGGTTGTGGACACAAT
2101	CCTGGCTTTTCACACGCCAAGAAA
2102	CACTCAGCGTAGCCTGAAGCCTGG
2103	GAATTATCGACCGCAGCGGTGTCG
2104	GTGACATCACATGGTGGCCGAGCG
2105	AGCACCTTGCCGAGTCACCAAGTGA
2106	TAGGTTGCAGGAATGGTGGGCACC
2107	GTCCCATACGTGTGGTACGCGGAT
2108	TCGGATACTCTCGCGTGCCACGGG
2109	CAACGTTGCCCCCTAAGCCCAAAT
2110	GTTAGGTCACCGCGGCATATCCTA
2111	GTTACCGGCCTCTACTTGGGTTT
2112	AATCCGCGTCTAGGTCATGTGGTC

2113	GCTACGCCTCTGGAGGTGGTACCC
2114	CAGGGAATGCTACAAAGGGTCCAA
2115	AAGGGTTAGCTGCCCCGGTTAACAG
2116	CCTCGCAAGCGCGATATTTATGCC
2117	GCCTCCCGGTCATGGTCAAGGGAA
2118	GCTGTTGAGCGGCGACCTGTGCAC
2119	CGCTGACTTAGCTCTGATGTGCCG
2120	TTCATGGCATTTCATCACGAAGGAA
2121	TAGTGTTATGCCCCGCGTGTGAATG
2122	CATGTAAGGGCACGGTCGTGGGCA
2123	CAGGAAGCTCGCTCCGTGATGCAC
2124	CCTGCTGATAGCAACCTCACTGCA
2125	ACTACGAGGGGCAGGGTCTAGGCG
2126	CATAATGTGGGTGCTGACGCCGAT
2127	TAGCGAATCCACACAGAGCCGCTC
2128	TCGCGAAATCCCTAAATCCTGTGC
2129	TGGCACGAATCAAGCCACCAACTC
2130	GCGGACCGTCTTTGCTATCTGACG
2131	AGGCCCCGCCTTGTAAATTGGTCAT
2132	CTGGTCCCATACGCCGCTGACTAG
2133	TGCTAACTGCGGCCCTACAGAGTC
2134	TGGTTTTATGTTGCGGTAGCGTCCG
2135	AGCTCAAACCTTCTCCACGGGATG
2136	CGCGAAGATAGTGAAATCCGCATC
2137	GAGTGAAACCTCTCGCGGGTTGCA
2138	TCGAATGCTCTGCAGTGACGTCAA
2139	AGGTGGCAATGATCGACGACCCTG
2140	ACCTTAACACAGCCGACCAGGTGA
2141	GTCCGGAGCCGTGCAAAGCAATAA
2142	TCTGCCTGACTGCTACATGCTCCC
2143	CTTTTGGGGATTAGAGGCCGACAA
2144	GGCATAAAGGCTTCCGTTCTGTGTC
2145	GCGGACCGTAAAGCGGGCAGATAG
2146	TTTCAAGAGTGCATCGAATCCACG
2147	CCGGCATCCCTTCTCGCTGTTGCC
2148	ACACAGAGACGCGAACGGAGTGCA
2149	AGCGGCATTCTCCCACTCGTTACT
2150	GGAGCGTACTGCGCCTCGCAAGTC
2151	AAACCCGAATGACACGGCAGATAA
2152	GGTCGGGTCCATATCCAAGTAGGG
2153	AACCAGCGGATCGATAAACGACA
2154	GGTGTCCACCCGTTAACGCCGTA

2155	AGCGCGACGTGGCTTGGCGTTAA
2156	TCCCACGGCTATAGGTCCAACGAC
2157	ATCAACGAACGATGCCGTTAGGTG
2158	GAGGCTAAGCCGTATGGCCGAGGC
2159	ACGGTCCGAAATGGTTAGAGGCAC
2160	ACGCAAACCATTCCTCGAGTAGGC
2161	TTACACGCTCGCTATTGGGCCATA
2162	CTCGGCACGGGTTTAGAACGCCGG
2163	ATTCGGTAAGGTATCGGGCTAGCG
2164	AGCACACCGTTATACATGACGGCG
2165	AGTCCCTGCCGTTGCTCATGGAA
2166	GGGCTTATGACCAGTCAGGTTGGA
2167	GGTCACCACACGAGTGCCTGGTCT
2168	TTGATCGTGTCTCCCGAAACCCTC
2169	ATTGTCGCGATCGGCATTTCTTAA
2170	GGGTCCAACGACTTCTCGCTGCTG
2171	CAAATTCCTTGGGGGCCATAGTGG
2172	CCAGAGTATCCGCCGTTAGACGGT
2173	TCCTGCAGATCATCTCGTGTCTGG
2174	TGCGGGAGATTTGAACAAGCTGTA
2175	TTAGACGCCGAGCTAGGCAACGTC
2176	TTTCGGCAGAATCTCCGATTCAAC
2177	TGGCGAGCAGACCTACAAGACAGA
2178	GGCGACAGACCGGTACATCGGCCA
2179	TCTAGACCTGCGTTTCGTGGGACC
2180	GCCGAGCGTGGTACCATACGTTCA
2181	TAATCACACCCGCTTTCTGTGGCT
2182	GGCCGGAGCCATTGGACACTTCTT
2183	CCTGTAGACCTGCATGGATCGCTG
2184	GTGTGTGTGTCTGCGTTGGGGCAC
2185	ATCGCCGTTCCCGCAAATAAGCA
2186	TGGATCAACGGGGTAGTGAAAACG
2187	AAGCGACGATGCTTTCTTGAGCTG
2188	CACGGGCACGTGTTCTACGCTTGC
2189	ACGGGCTGGGACAAGAGCTAGAAA
2190	GGTAACTGGCTCCGCTCTCACATC
2191	ACTCTGGCTGTTGGCGAACGTGAC
2192	GACCGAGGACCACTCCTTGCTCTC
2193	AGTAGCTCTTGCGGCCTAACGGCA
2194	TTCTTGTCTGGGGGAGAGCAGTG
2195	TTAGCAGGGAGGTTGTCGGCTCAT
2196	TCGGGAGAGGGCCTTACCAAAGC

2197	AGAACGTGGATTGTACGCTCCGCC
2198	CTTCACAGCCTGGAGCCACCAATG
2199	GAGATCGATGAAACGCACCAGCGG
2200	GGGTCCAGAGTTGGTGTGGGATAA
2201	CCGTCCACCCCAGATAGGAATCAC
2202	TGCCTCGCTTCTGTGAATCTACGA
2203	GATCACAGCGTCCGCGCATAACGG
2204	ATGACGCCTTACATGACGCACCTT
2205	GCGTGGAATAACGCCCTTAGTTCA
2206	GGTCTACCATTCTCGCCCGACCG
2207	ACACCTCTCTGGCGTAGACGCTCA
2208	GTAGAGGTGCTCAGGACTCGTCGC
2209	GTAAGCAGGAGGCGAAGGCGCGAA
2210	TCTAAGGGCCGTTTCAATCGACCT
2211	AACCTGATTTCAAGGGTCAGCCCGA
2212	GTCACGCGATTGGCCACCTATTA
2213	ACGATGCCGCGCATGTAACCTAGT
2214	TGAGAGATGTCTCGTCAACGCCTG
2215	GCATATCTCGCGGTGACAGACGAA
2216	TATCCTGGACCCAGCCTTGGAGGA
2217	GACCCAACGTCGAAATTGTGCGAT
2218	TGAAAATCGGGGCATCTAGTTTGG
2219	CCGCGAAAAGGATTTGTGTACGCA
2220	CATTCCATTTATCCGCAGTTCGCT
2221	CCTGTCTGTCGAGCCAGCGTCTAT
2222	TCAGCGCGGCTAAACAAGTTATGC
2223	ACGCCTACGAACGACCCAAGAGAG
2224	TGCGCATCTACCATTGTGTGGATC
2225	AAGTCCGCGCTCGCTCCTGTAATA
2226	GCTGGGTCATTGCTCGAGTAACCA
2227	TGGAGCGTTCTGGCAATGACCGAC
2228	CAAGTCAATTCTTGCCAATTCGG
2229	CGTTCATGCAAGGATCCCAGGTTA
2230	ATGCCAATAGAAGCTGGGGATGCT
2231	CCTAACTCTCCCTTGAGGCCGTTT
2232	ATCTCGGCGAAGGTTCCAAACATT
2233	GCGACAGATTACGCTGCGGTTTTT
2234	AAGCCCAGACGGCCAACACGTTAC
2235	TCAAGTTCAAATCACATCCCGTGG
2236	GATTGTCGTTCTGTCTGTGAGGCG
2237	ACCGAACTATGTTCCGGCATGGCA
2238	CGTCATCGGGTGTGCAATGCCGTT

2239	CGGACGGAGTCACGTTTGTGCACT
2240	TAAACAAGTCGTGTGCCTTTGCCG
2241	TAATTACTGGCCTGTGGAGCAGGC
2242	GGAGCGGCCCGAATGGTGCTCTTA
2243	ACTAAGCAAGGCTTGGATGTGCGT
2244	GGCAGCTCAGCGGCAGTACGCTAC
2245	GCGAGGCGAATTATCCGCGGATTT
2246	CATACGACACACCTTGGGGTGCTA
2247	TGCTTGGGCTTTAAACCCCGTTTT
2248	CCGGTTGAAAACGCAATATCGG
2249	AAACTAGCTAGCCGCACCCGCAAG
2250	GTTGTTCCACCAGTGATCACGCAG
2251	GCCGCTGACAAGATGATCATCGTT
2252	CTTTCATAAAGCCAACCGATGCCC
2253	CTGACTGCATCTCGAAAGCGGGTG
2254	ATTTCTTCGGAGAATCGGCCACGT
2255	CATTTGGGGCCCTAGCTACTGCGC
2256	CCGATCCCGCACATCCGTATCCTG
2257	TATCACCGGGAGCGTCTTATCGTG
2258	TAGGGCTCGTGCACCGATTAGAGG
2259	GCGTGGACTIONCGCTTGTCTAGGTA
2260	CTCAACGAACTCAAGGGCCGCTAC
2261	AGCCTGGTATCGACCAATCCTGCA
2262	TACGCGTTCTAGTTGGCCGGATCC
2263	TTTATGGGTTTGTGCCTGATGGGT
2264	GGGACCCCTAGCAACGTCACCTTA
2265	CTGCCTCCCCAGGAGTCATTGGAT
2266	AACCCCGCAAGACCAGTACCAATC
2267	GGTCACATACGCGCTAAAAAGCGC
2268	AAATGGCTCCGACCAGTTAGGGAC
2269	AACGCGGCACGCTTAAAGGTGCAT
2270	GATCGCACGCCGATTAACTTACA
2271	CCTCCTGATTGGGAGTGCGGAATT
2272	CGGAGGGTAATAGGCTCCTCTGCG
2273	ACAAGAACTGGACATTACCGCGGG
2274	TGTCGTCTTAAAGGCCTTTGTGCG
2275	GGTGACCATGTGGCGTTTTAGCTT
2276	CACGGTTGCGCACGGTACCAGAAC
2277	CCTTTATTGTTTGGTCCCCTGCCC
2278	GTGCGCCTGCATTCTACCGTCAAT
2279	GTTTACGTTGATGGCTTGCCGCCG
2280	CCGTCGGTGGTAGGACGTGAATGT

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2281	TGATCGCCCCAGAATCCCTGTGCT
2282	AAGCAGCCAAAAATCGGTTGCTTT
2283	CGACGGGACTTAGTAGCAGGGCCT
2284	CCGATTGCGGAAACGACCAAGTAG
2285	CCACCCCAACTCCAATCTTTCTCA
2286	GTGCAGTAGACGACTACCGGCGTC
2287	TTCGCCCATCGTATCAAGCAATTC
2288	GAATCGCGACTACCCGTCGGGTCA
2289	CCAGCACTCGCCATCGGTTATAAT
2290	CGAACCGTAGAACTCCGGTCGGTG
2291	GCACCATGACAGAGCCCCAGGATG
2292	TGGGCTACCGCAGAATAAGGGTGA
2293	TGGCCTGTCGTGTCGAAGGAAACA
2294	GCCTCACCGATAGCGAGCGTTTGC
2295	GTGCGCGCCGGCTAAAACGAGACA
2296	CCGCAGACGAGTTTCTTGTGACAG
2297	GTTGCAATCGCGTGCTAGGAAGC
2298	TGTTGTACACATGCATCCGGTGA
2299	CACTGAACACGATATAAGGGCGCG
2300	CGCGATGGTTCTTAGCAAGACGAT
2301	TACACCAAGGAAGAAATGGGGACG
2302	CGTGCCTTGCGTTTTAGGTGCAGC
2303	GTCGTTTGTCTGGGCATTAACGGC
2304	CAGGCTCTCGTTCGGTACAAACGT
2305	CGGACACTGTTTCACCAGAACCCA
2306	TACCCATGATGCGGAAGAAGCGTA
2307	CTGTCCTTAAGCGGATGAGAACCG
2308	CGGGAGATGAGAACGGTTTTGTGC
2309	TAGATCGCGACTGTACTCAGGCCG
2310	TAAACAGTTCGCGCGACTGTCGT
2311	CGAGGAGCTCCACATAAGCCCAAT
2312	TGGCTAGGGATGGGGAATCATCTT
2313	AGGATTGGGTGCCTGGATGCATTG
2314	TGTATCTACCGGCCTGAAGCAGGT
2315	TCCCTACGCGCATGACTCGCTTAC
2316	TGGTCGATCACCTGTGACAGACGC
2317	TGGGGGTAGTCCATGCATCAATTG
2318	CCCTGCCAGGATTACTATTCCGGA
2319	TCCCGCACGGGGAATTTAAGTAGA
2320	GTGATGTGCAGGAACCTTGTGCGC
2321	ATTAGGCATGCATGCGCTTCTCA
2322	TTCGGCGCTAGTGGACGCCGTCAA

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2323	GAGCTTCATCTCATCAGTTCCGCG
2324	GACAACTCCACTGCTCCAATCGCA
2325	GGCCAAGGATGGACCTTACGATGG
2326	GGTTCGGAATTTGTCACCGCTTC
2327	GCGCTGGATAGTCTGCGAGAAGCC
2328	TGAGTCCAGTGCTGCCACCATGAA
2329	TTGAATTGGGTGTCGGAGCGTTCT
2330	CGGCGGGCAGACAATGCTTTGAAC
2331	GGGTCTGTCAAAGAGGGTGTCTGG
2332	CTTTGTGCAAGACGAAGCACCTT
2333	ATCGAATTCGAGGAGGTCTCCAT
2334	TCCGACCCTCAGAGTCGACTCATT
2335	ATCAACGGCCACCTCCTCGCCGAG
2336	AGCCACGGAATAATTCCGTCCACC
2337	GATCGCTTGGTATCGCAAAGACT
2338	TCCACGCCTTACCATCAACTGCAA
2339	GCCAAGCGATAGGCCAGAACTCAG
2340	AGCGTGTGGGTCATTTTAGCACGA
2341	GTTATGCGCGGCTTACGAGTTCGA
2342	TCTGTCCACGTAACCTGCCTGCAG
2343	TCGGCAGCCAATGATCATACCTCT
2344	TAAGCCCGATCCGGTCCTGTGTTT
2345	ACATGGCAGACTAACAGGCCTCGC
2346	CATGGCTGCACTCTAAGTCGAACG
2347	TCTTCAACCCACGCGGAACGATTG
2348	CTCGTGTCTCCAGAGGATTGTCCC
2349	TGAAGGCATCAACCCAGAGGATTT
2350	ACAGCTCGAAGGCAGCCACATTGG
2351	ACAACGAGTACCGCGACAGAAGGG
2352	ATAACCGAAAAACCAGCCTGCGAT
2353	ACAACTCAGCACTTTGACGTCCA
2354	CGGGTTACTGGGTATACCAATGC
2355	CATCGGTTATCGCTGCACGCGCGT
2356	GAAGGAATCCCGGATAGTCCGTGG
2357	GCATGGTCTCAGCCAAAGAACCTG
2358	AGCCTGCGACGTTTCCCGACAGAC
2359	AAGAAAGGCGCACGGGATCGATAT
2360	TGTCGCGAAGCCAACTTTCAGTAA
2361	GCGGCATGCAAGGTAGGTCTGGAT
2362	GGTGGCCATCTCCTCGAATTGCAT
2363	GCGTGCATAAGTTGCACATTGTGC
2364	TTGAGGTAGCGTTTTCGCGCATAT



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2365	ATCCCACTTGTGAGAGGGCGCATT
2366	CGGTCAGCGAGCAGACATCAACCT
2367	GCGTATCTTCGGGTCGAACACTTG
2368	ATGCCATTGAACTCGCACTTTGCG
2369	CGATTCCCATCATAATGTGGGTCC
2370	CAATTTGGATAATCCAGCCACGCC
2371	CGGCTTACCCTATGATTCCGTGCA
2372	GGTGGACCATGCGCTGTGGTATGA
2373	TATTTGTGGAAGATCGCAAGCGCC
2374	GTCAGTGGGTTTTGAGAGCCCGCA
2375	AGGGGGTCGGGAAATCTGACAAAA
2376	TGCTTGCTATCCGAAAAAAGCAGG
2377	TTATCGGATCAAATTCGGCTTCGG
2378	TGCAGCAACGAGTTACCCGGACTT
2379	TATACATGTCCGGAGGGGCACCCA
2380	TGCAAAACCGGAGGATGAACCCTT
2381	TCGGTCTAATGTCCACGCAGACAC
2382	ATGTGTTTGCCACGCGCTCCTATT
2383	TGGCGAGGCACGGCTCTAATTCGG
2384	GCGACGACCCGAGCGACTTTTACA
2385	CTCAGAGAGTCTATCCGGCGCCCT
2386	GGAACATCTCCTGGGTCCCTCAGA
2387	GCAACGCAGGGAAGTACTTAGCGA
2388	TGACTTGGGCGGACAAAGAAACGC
2389	AGATCATCGGGACGCTTCATGCTA
2390	CCCTTCTGACCGCTAAGGCCATAA
2391	CGTGAGCCGTGGGGTGTCTCTGTA
2392	TACCTTGGTCGTCTCCGCTTTTGT
2393	TCGCCGCAAATGCTACGTGAAAA
2394	GAGTGACCTAATGGCTGCCCGACT
2395	AAAGGAACTTGCCAACCCTATGG
2396	TGTTTTCGCACTCCACCTAATCGC
2397	CAATGGGTTTCATAAGGGCAGGCA
2398	GCCTAACACACAAGGGTCCCTCTG
2399	CGTCATGCGGTCCGAGGATCGATC
2400	CCACACGGGCACGGAGTAATATCT
2401	CATCAGACATAGGTGCGGTGCCGA
2402	AGATGAAACCAAGGGAGGACGCAG
2403	GGCTACCCATAGGCTCAGCAGCAC
2404	GGCTTGAGAGGTGTGTTCTCGAC
2405	TGTGTTACGGCGAATGCAACAGTC
2406	CGATAACAGGTGCGGCCGTTACTA

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2407	TGATAAAGTGAGGCTCCAGCGCGA
2408	AATTGTGCACGGATCTGCACGGCG
2409	GCCGATACTGAGCATTTCACTGCC
2410	GCAATGTACTGTCACCAGTGGCGA
2411	GGCATATCGGTAACACTTGGTCGG
2412	GGGTCTCAAACCAGCGTGGCCGCT
2413	GTCTCCGGGACCATTGAGCTGGAG
2414	GGCCTTCGGCATTGAGACGGGTTG
2415	CGTGATAGGCCACAGCGCTCAATT
2416	GGCAGGCCCCGCGAGGATGATTAAAC
2417	CGGGTATGGTTGATAACAGCGTGG
2418	ACGACGTCCTTGGGACCGTATTGT
2419	CTGATATCGAGCCTGAGCCTTTCG
2420	TCCCATTGGCCTGTATGCTGGCCT
2421	GTGTCGTCGATTGTTTCATCGACG
2422	CGAAAGCCAGTAGCCGATTGCGTG
2423	GGTTCGGCTTATTCCACTGCGACA
2424	AGCGAGGGCTAACTTTTAAACGCG
2425	CGGCGCTGATGACGGGACTCGATT
2426	TCACAGTGCTCGGCGTAAGGACTA
2427	CCCATTACGAGCACACACCATGGC
2428	GGCCGCTAATCTTTACGCATCACG
2429	ACGGCTTCCTAGTGTCCAGCCCTT
2430	CTGTCAGGTCCTACCCAATGGCTC
2431	CACAGCCCATCCCCTGAACTGCT
2432	ACAAACGATACACGCAACGCTGTG
2433	TGGCGGCCAGCTAGCAGGCGAAGT
2434	ATCTCGAAACGATGCGTGCCTAAA
2435	ATCTCGAGAACAGCGTGCGTGCGG
2436	GAAGAAATCCGCCGACATCTACGG
2437	GCGGAGCAACCTTGGCTGTTTCTA
2438	CGCGTTCCGAAGACTTGTTGTTTG
2439	TGACCTGAAGCCCATCCATAAGCA
2440	TGGTATTCATTCCGGATAAGCGGG
2441	GCGTTGCGGGTCATTGATGCAAAC
2442	ACCGCTTTCTGTGTAGAGCCCTGA
2443	CAAATAGACAATCGCAGCTTCGGG
2444	TGTCCTGACAAATCAAGGTGCAGG
2445	AAATTGCACTCGCGGAGATTTCTT
2446	TGACGCCCATTTCTATATGGTGCA
2447	TGTTCCGACAGGGCACTGCTAGAC
2448	TCGCTGGCTTGGGAAGGCCTTCGT

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2449	GTGCACCTCCGTTGGCGTAGAATG
2450	CTCATTTGGGACCGATCGGGTTGC
2451	GCCAGTGTCTGTCAATGGATGGGA
2452	TTGCCCAGGAGGTTCTGTGTAATG
2453	ACCCGCGAACCAGACGCACTTCT
2454	TCCGTGCGATTGGTCAAGGTTGAT
2455	AGGGCGTCTCGGTTGAACCTCGGT
2456	TGACCGTTCAAAGAGCAAGCCAAC
2457	ACACTCACCTGCTGTCCCTGCTGA
2458	GCGTTTAACTCCTTGGGTGGTGGT
2459	CGCCTGCGCAGGTAAGTCTCCGCA
2460	AATCGAATTTCCAGCGGCTGTTT
2461	AAGCAGGTGGGATCCTGGGGATCA
2462	AATCCCAGACTCGCTCTTCGTGCT
2463	ACGGTTATAAGGGCCGGCTGCGAC
2464	TACGAGAGCGGGCTTAGACGTGCG
2465	GCGATTTTGACCCACGGTTATCGA
2466	AGCTGTATAATTTGGATGGCGCGA
2467	TCCGCGAGTCTTAGCCGATTGAAC
2468	GGCATCAGCTCCGTAAGCCGATAG
2469	TGTTATTGGCAGTTCGAGCGACAG
2470	GCGAGCCTTTTGTCTTGGGAAGAG
2471	AGAAGAAAAGGTCAGCGTCGACGA
2472	CGGGTCGACCCTTGAAGCATAACC
2473	CTCGGTTTTTCAAACTTACCGCG
2474	GCAGTCCTATCCGGAGCCTGACAA
2475	AAGGTGCGCTATTTGTTGTCTGGTC
2476	AGTGAATCCATGCCGACACCTGA
2477	TACAGGCGTAATTCCTGCGAGGGA
2478	CCGAAGTGCGAGAAGCACGTTGTT
2479	AAGGACTGGTATGGCCGGAGCTTT
2480	GGACACCGCCAACCTCATAGTTGC
2481	AATGGTGTTGCGCTGGACTACCAC
2482	TAGGAAAGCGTACACGGGAATCCG
2483	TCTCACCCCAATGATGAGGACGTC
2484	CGTGTCCGTGTGACACTGTCCATG
2485	TCCAGGCTGTTGCGGATACGGTAG
2486	GTAGGCAAAATGGTCGCGATCAAT
2487	ATCTCCGTGGACCCGATTGTGACA
2488	GAATATGCCGTCAACGCTATGGGC
2489	TTCCGGAAGCGTTTGGTAACCTTG
2490	TTCGATAGGAATACCAGGGCCTGG

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2491	GGCCATTTGAGGAGGATTATGCAA
2492	ACCTTCTGACCTGGACTTTTGCG
2493	GACCAATCCGCAGTTGAGCAACAG
2494	TCGGCCACTCACCATGAGTGTAGG
2495	AGCGCTCACATGTTGAAAACGGG
2496	TAACGCAAAGGCGCGATCCTCGCT
2497	TGGGTGGGCCAAATATTACTGCAA
2498	GTCCTCGAAAGGGGCATCCAAACA
2499	CCCATCTGGTGGGAGGCGTTATCA
2500	GTGCGCGGTCTGCAAACCTGCCAT
2501	TGTGTTGCCAACCTAGGTCATCA
2502	CTGATGCTGTTCTCGTCGGTTGAC
2503	AAGCTGCAAAGGTGAGCGTGGCA
2504	TCTGACGCGTGCTTGGGAGTCTAT
2505	GAATTACTTGGAGGCGCCGTGCAA
2506	GATTCTTCCCGACCTAGGTTGGCC
2507	CGCAGCGTATCCCATGTTGCTTGA
2508	GAGATGGAATTGTTGCCCCAAAGA
2509	GATGCCTGGATCGGTCTAGCGTCA
2510	GCAGCGACTGCTAAGCTATCTCGG
2511	AGGGCTAATTTACATCGCCTTGCC
2512	AAGTGACATCCTCACGAAGCGAT
2513	TCAGGCAGCCGTAATTAATGCGC
2514	CCACTGGGGAAATCGCACTGTTGG
2515	TTGTCCAAAGCCACCTACGACAGA
2516	TGGGCGGAATAGATTGGGTGTCTT
2517	TAGAATTCGCCTCTTCTAGCCGCC
2518	CATTACTTCCTGCAGATGCGATGC
2519	GGAAATGCTAGCTGGGGTAATCGC
2520	GCCGCCACTTGCGAATCTACATCT
2521	ACAATAGCGGACAGCTCGCCAGAT
2522	AGTTAGGCTCTCGGTGCGGTCCAT
2523	TGGGCCTGAGAAGCGGTTAATAGG
2524	ACGCTCTGAGCGACGCCTATCGTA
2525	CCTGGTGATCGTGTCCCAGACTCA
2526	GCGTGTCCATTGCTTGAGGTTTC
2527	ATCCTGAACGGCGATGACCACCAC
2528	TTACGTTTCTCACCGATCAACGCC
2529	GCCGTCTTGAGTGGCTAAAAGGCA
2530	ATCTACGATGCGGCTCGAAGTGTT
2531	AACCAAGACTCGTCCCCAAACGAA
2532	AACTGCGGTGGTGGAGGCAGGTGC

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2533	CCTGAGTGGTCGGGCTGGAAAAAT
2534	TGCGATCTTCTCCACCTACAGCGC
2535	AGGCGCTTAGAACCGTGAAGGCAG
2536	TGGAAAATTTTGGGAAACGCTGGA
2537	CCAGCGCCGCACCTTCTCCAATAG
2538	TAGACGGCTGGCGAATCTTACGGT
2539	TACCATACAAGAGAACGAGCCGCA
2540	GTAGCCGAGAGCAATTTTCACCGC
2541	GCAAACCTCCCCTGCCCTTTAGCCT
2542	ATCCCGCTGATAACCGCCAGGATA
2543	AGTCTCAGTTCGGCGCAACGGTAG
2544	AACCTACAGTCGCCGCAATGCATT
2545	ATACACGTTTCAGCCGGCAACAAT
2546	ACGACGGGACGTGCCCTCGTTGAT
2547	AAGTCCAAACTCGAATGGGGCAGT
2548	GATTTATTGGCGCGGTAACGACCT
2549	TGTTTTCAGAGGCTACCCTGCCAT
2550	ACGGTCTCAGGGAAATGCGATCTC
2551	GACTTGAAACCGCCTATGCCCACA
2552	CGATCGGTTGTGTGCTGTCTTACC
2553	AGTAGCACAATGCCTCATTTCCGC
2554	CTCGCTATCTACGCGTCTCCGAAA
2555	AGCCCGTTACGGCATCTAGGATTC
2556	TCGCGATGGCGAGAGTTCAGAATA
2557	TTACAGGATTCCAAAACCCGCAA
2558	CGGTACCAACGCGCGGGCATATGA
2559	TGCCAGTATTATCCGTGCCAGCCG
2560	ATTCAGACCTCGGGACAACCTGG
2561	GAAGTGCGCGTAACTTAGGGAGCC
2562	TTGGCCAGGTCATCACTCTGCCAT
2563	ATCGGCCCGGTATTAGCTGCCCTCC
2564	CGCAGGTAAGGCCGAGCAATGTTT
2565	TTGGGAACGTGCTAGGCGGCCCTC
2566	CCGCAAAAGTAGAACAGCCTGGGT
2567	CATCTCGGCACACTGGTGCTGTAT
2568	ACGCGTAAATCAACGACGTGGTCTG
2569	CGTAGGTGGTAAATGTTGGCCAG
2570	GTTGGGATGCTGCTTCACTTTGGG
2571	TTGAGCCAGAATAAAACGGTTGG
2572	AGAGATATTCGGCCTCGGTCGAGA
2573	CGACAAAGTTTCTCGCGAGCAACT
2574	ATTGCCGCGTCTCGTATCAAAGA

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2575	CGGAGAATGGATGCAGGTTCTTCG
2576	TATAATCATTGCGACTCGCCCA
2577	AATTTTCCCGATTGAAGAAGCG
2578	TCGCATACTTCGTCGGCGAGTATT
2579	CGTGAGCCGTTCTCATCCAAGCGG
2580	GCAGAATCGAATTGGGGTGGGTTT
2581	CTCTCGGTTTCTCAACCGAGCTCG
2582	GACCAGTTAGTGCAATGGTTGGCG
2583	TTCTCGCACAGCTAGTCAGCCGAT
2584	CCAAGTCTTGCGTGAGCGATCCTG
2585	GCGAAAGTGGCTCGTATTTCTCCA
2586	CCTCGGGACTGTCCGACTGAAAAA
2587	AGGCGAGTGACGGCTCATCCATG
2588	GCGGCTCTGCCTACGATATTCACA
2589	TGCACCTGTCTGTAGATTTGCGGT
2590	CATAAAGCACGGACGCGACTTGAT
2591	CCCTCAACGTAGGGCGTGACTTTC
2592	GGGTCATCGTGCAATTATGCCGTA
2593	CCCGGATAATCCTTTGTCCAGCCG
2594	TCCGATAAGCGAACTCACATGGGT
2595	CCTGCTGGTTCGGTCGTAAGCGAA
2596	GAGGCACCAATCGGTCTGAAAATG
2597	TACGAAAATGGTTGCGCCGGGTCT
2598	CCCAAAGATCGTATCACCACCCAA
2599	AATTGCCGGAAGCAGTCAGAATCG
2600	CCGAATCAGCCGTATTTGCTGGAA
2601	CCCGCTTATCTGTACTCGATCGCA
2602	TTTTGGGGATCCCTATTAGGCGCA
2603	AGTGACAGCGCTCACCACGGTCCC
2604	CCATGAGTGTTTCGGGACATCGTA
2605	GCCACATTCTGCTACCTCCGTGTT
2606	TCCTGTGCTTTGTGACGTGCTAGG
2607	GACCGCATATACACCTGATGGGCC
2608	GTAGGCCCGTCGTTAACCATCTCA
2609	CGGCTCGCGAAATGGAGTTTAGCG
2610	GCTGATCGGCTTTTCACCGCTATA
2611	TATCAAATCGTTGGCACGCGACTA
2612	TTGGCGAGGATCCCTAGGCGTACT
2613	AAGTCCTGAGGCCGTTTCGGTTTCT
2614	ACTCCGGACATCTCGGCCAGAGAT
2615	CCAAGGGGAACACAGGATCGTAGA
2616	GTGGCCTAAATCCGCCTTCTCAAC

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2617	CACTCCGTCTCGTCCATTAATGCG
2618	TCAAGAACCCAGTGCCGGTCAGCA
2619	GAATCAATTTTCCAGGGACGGGAC
2620	GAGAGCATACGCAATGTTCCCTCC
2621	ATCGGTGTGCTGGAGCGCCAGAGT
2622	GCCTCTCCTATGACGATGACCCAC
2623	TGGGCGCGCTTTTAAGACTACATC
2624	CGTTGGGTACCGTTCTATCAACCG
2625	GCAGTGAGCTGGGTTCAATGCTTC
2626	CATCATCCACACAGGCAGGTGTGT
2627	AGACAAAGGTCCCCATTGCGAAAT
2628	ATACTCGTCGACGAGAAGCGGAAA
2629	GCAGAATGTGTTGTCTTCGCAGCC
2630	CACCATGCCTTCATCTTGGCCTAG
2631	ACTCTTCAACGCCAGGTTAAGCCA
2632	GCGACCTGCGGCGTGTGTATTCTC
2633	TCGGTGTATGCACCTTTCTCCAT
2634	ACCGTCGAATCTTGCGGCCAATGT
2635	TAATGCATGCTCCCGGCTCACGTT
2636	TCTGTACACACCACGTCGTGCACA
2637	CATGGGGTTGTCAGACGACACCTA
2638	AATCTGATGCTCGCTGTAGGACGG
2639	TCGAAACCGCGGAAAGGGTAAAA
2640	CGCTAGGGCCTAGGGGCACAGACA
2641	TGGGGGACGGGCGTCTAATCCTCC
2642	AGGCATGCACCCATGCTGCCAGAG
2643	TCCAATGGCCTGTCAAGCATAAA
2644	GAACCTGAGCCTTTGCTAGCACGA
2645	CGAATTGATAGCGTTACGGGCGAA
2646	TTGCACGCGCGCGAACGACTATTC
2647	TGCGGTGAAGCAGTCCAAGGTCAG
2648	TGAGGACCATCCAATGGATCGGTT
2649	TCGGTGATTGGTAATTTGGATCCG
2650	GCGGGCAGGTAGTTTGACTGGATG
2651	CAAGCACAAGCCCATGAAATTTCA
2652	CGGTACAGCGGATAGCCAAGGATA
2653	CCATGCTCTTCGCTGCAGCATACT
2654	CGCGGCAAAGATTAATTCCCGGCG
2655	GAAGACCCGTCCGGGTTTCCATAC
2656	CTGGCAAGGAGGATGTGGCTCGTG
2657	CTGTGCAGGGGGTGGCTCTGTTGA
2658	TTCAATAATGATCACGAGGCCCCA

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2659	TGGTGATGCGAAGCCTTACCTTTG
2660	CTGCCACCATCTACGGCGCAGTCT
2661	TTTGCCCAGCTCTCGCAGAAGTTA
2662	AATTCAGACGCCACATCGACGGTC
2663	CCGTGGTCTGCCTCGATTACCTAC
2664	GGCGAGGAATTTGGAACCTTATG
2665	ATCCGATGATCAGATACCGGCTGG
2666	CCATAGACTAGCGCCAGAGTGCCC
2667	TGTGGACCTAGAAAATTGCCAGCC
2668	GAATAATCATCGCGGTCCTCATGG
2669	GGGATTGGCTCTTGGTTGGAAGAA
2670	ATTGTGCTTCTCGAACTGGGAAA
2671	TGCCCCACCCCGTAAGTCAATAAT
2672	TCAGGACCGACGGTGCACCTTAGTG
2673	CCAGCCGTCACAGTGCAATTTCCG
2674	CTTAAAGAGGCGCGAAGCACAACA
2675	TACCGCTCGTCGCGATCACAATGA
2676	CCGAGTGCGCGAAGTGTCTATGTG
2677	GCACCAGTGCCCGATCAAAACGTA
2678	TGCAGGCTTCTCAACGGCTGGGAG
2679	CTCCGTACGTATCCCGCGTGATAC
2680	GGAAGTGCAACTTAAAGCCCCGCC
2681	CGAACCGGCAGTCGATCGTTGCAT
2682	CCGTTAGTGGTCGACAGTTCGGTT
2683	TCAGGCTACGCCCTCAGCACTACA
2684	TATACGGGCCGAGGTCCGTATTCCG
2685	CCAACGTGTGACGAAGGGCCATTG
2686	CTGCTCAGCGGTGCTTGAAAGACA
2687	GGAGATTGACTTCGCGTTTCACCA
2688	ATGGTTCAGAAGGTCGTGCGGTT
2689	GAGTGGAGCATTCTCGGCCCTCAA
2690	TGGATTGGAACCAATCCCGCACAA
2691	TGCTCTTGTGGTCACTCGAGAGGA
2692	TTGGGAGCACGGTTACCGCCTGTG
2693	CAACGCGAGCTAACGGTAGTTTCG
2694	AACGCTGAGCGCTCACCTTCACCT
2695	CCGTCGTAGATCTGGAGGCTTCAA
2696	GGATGGCATGGGCACACTGTAACC
2697	TCGCTCGTAGATATCCTTCACGCC
2698	GGAGCAATACCGCGTCCAAAACAC
2699	CGGTGTGCTTCAAATGCCAAAGGA
2700	TTGTTCAGACTTAGGCGCTGCCCA



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2701	CGGCGGTACTCTTTCCACTGTCCT
2702	AAGACGATTGCCCACGTGCCAGAG
2703	AGGTGAGCGCAGGCATATTGCAGT
2704	CTCGGGCCTGTACAGCAAAGCCGT
2705	TGCGCGCTAGTGCTGCCTATGATC
2706	CCATCCTTTGCCTTGAGGGTAAGG
2707	AACAACAGCGTAAGACGGACAGGG
2708	GAGGCGGTCGAGGCTCACAATATT
2709	CGAGGTTAGACGCCTATGACCCAC
2710	AACTTGCTATACCGGGCGCAGCAA
2711	CGCGGTGAATCGCATACACAGCGC
2712	CACCGAATCAAGCCATATGGCTCT
2713	TTCACAGCTATCCTAGGCGCTGCC
2714	AGAAGCGCGAAGTGACCCCGCAT
2715	TGCATGGTATTTGCGTGCGATAGG
2716	GGCCGGACCTATGTGAGATGAAA
2717	TCAACCTGAGTCCTGATCCCAAGC
2718	TGCTTACCGTTCAGGGAGGCGTGT
2719	GGAGAGTTACGCGATGAGCCACCT
2720	CGGTATGCGGTGTACAGCTTTCGT
2721	GTAAGCCGGGTCTCGTGTGCGCGT
2722	GCGTAGTGCGAACGCCCCGACCTA
2723	TCCTCGCGGCTTACGTCAAATTCG
2724	CGACGTTCAAAGCGGGAGAGGAGG
2725	CGAGGCACCCCGACATGTTGAGAT
2726	CTATTTTCGTGCCGCGTCGGACAAG
2727	GGCTGCTCAGTGACGTGTCAACTG
2728	ATCACTCGTGCGTACCCGACCGTC
2729	CGAGATGTCCTATACCGTGCGGAA
2730	TCACACCGAGCCCCATAAATGAAA
2731	AGCTACGTGTCTCGAGCAAAAGCG
2732	TCAGGGCGAGTTTTTTCAGCGGCG
2733	TTCGTTCTGTCTATTTTTGCCCGG
2734	TGGTATGCCCAGGATCCAGCCTAC
2735	TCTCAGTCGTTAGGCCAATGGCGG
2736	AAAGATCACCGTGGAGCGATCGGC
2737	TAGCAGGACTTGCACTCGTGATGC
2738	TGCCCACGGTACCGTTCAAGGCTG
2739	TGAGGTGCGTCGCCCTAAGTAATG
2740	AGCAAGGGTTACAACCCGCAACCC
2741	CACAACAGCCAGTATTCGCCACAA
2742	GGCAACACCATACTCGACGAGCTC

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2743	GGCTGGATTGACAATTTAGCCCCT
2744	CGTGAGAAATGCTACACGCGTCAG
2745	CGCATCTGCCCCATTTTGTTCCTT
2746	GTCGGCCTAGTCGGCAGAACGGTG
2747	TCGACACGCGTAGCAGCGTGACACA
2748	TCCCTCACCTTCCAAAAATGTGCT
2749	GGGCAAGAACATGAGAACAGACCG
2750	TCGTCCTGGTACGACTTGCGTAGA
2751	TGGCGGTTGCATGTGATGATCAAG
2752	CCTCGCGTGAGTAAAAACCGTCCG
2753	ACTCCGCCACAGAAATGCGGCCAG
2754	GTGTAGAGCTTGGGTAGCCCCGTT
2755	CGCAGCATCCGAGTTAACACACAT
2756	ATGAGCCTGGGATGATCCGCTGGT
2757	CCTGGCATAAGTGCCGACATGCTT
2758	GCGCATGAAAACTACGACGGACG
2759	AAAGATGGGTGCGATGGGAGCGTCT
2760	ATCCTGGGCACGAGCGGATTTATC
2761	TCACCGCATTTGATAGTTACGCGA
2762	TGGTGGAGCGGACTCTGGTGTTAT
2763	CACAATGAAAAACAATGGCCCCA
2764	CCTTGCCGCGCTTGTTGGTACCAAC
2765	CCGAGACCTTTGCCACACGAAAGA
2766	ACCGCGGTGTACACCTGAGCAGGC
2767	GTCGTACGCTTACCGCAGCGGAGA
2768	TCGTAATTTGACCGACACACGCAG
2769	CCTAGACGGATACCCTGAGCGGAA
2770	AAGCGACAGCAGAGGTTCAAGTCGC
2771	GCGTGGACGATATCACCTGGGCGT
2772	GTCGGAGAGCCAGTGGTACGGCTT
2773	TACCCTCCGGACCAGCTGTAATGA
2774	TATCCGCACGGTATAGCAGTTGCA
2775	CATCAGTCGGGCTACCTTCAGCCT
2776	CGGATTAATGCCTTTCCTCGGAAT
2777	TTCGTCGTGCCAAGCTAATGCAAG
2778	CCACTACGGATCAGCACAGGTGTC
2779	GGCCGAGACCACCAGTAACAGGTT
2780	CGCGCGGAAGCATTGAAGTTACTA
2781	TCGGCTTACCGCTTCGTCTGACTT
2782	GACTGACGTCAAGGCAAGCAACAC
2783	AGAGGAAGGAGGGGCTGTGACAGA
2784	TTCCAATGCGAGAGATGGCAGGCT

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2785	AAATGGGGTGCTTCGAATATGTCG
2786	GCTGTCGGATTATTGCACGCCTGT
2787	CCGACTTTGTTTATGTTGCTGGCG
2788	GCTGCGATATAACCCGTCCCAGAA
2789	TGAGCTGGGCGTCAACTCCGAAGA
2790	CCCAAGCATCCTAAATCTCCCTCG
2791	CGACAGCAATCCACATGCATTCTT
2792	TGAATGGTCGGGAAACCAATGCAT
2793	CTTTGCATCGAGATGCGGGGTAGC
2794	TCCATTTCTCCGCAACTCTCAGG
2795	CCACTACGCCATCCTGACAACGAG
2796	TAGTAAGGCCAATGTACGCCGTCC
2797	GTCATGCATATGGGCGCTGTTTTC
2798	ACCGGTAGACGTTAGCGGGTTCAA
2799	TTGGTTCAAACGGCCACACGTCTC
2800	GACACAACTGCAAGGGAGGCATG
2801	CTCGAGCGCTGTCATCATATCGGC
2802	GCGGCTAAGGCACAAGTAGACGTG
2803	ACAGCCTAAATGGCGCAAGACCGA
2804	GCCAAATGCTTGGAATTTGCTTCG
2805	CCGATGATGTAAGCCGTCGGCCCT
2806	AGGAGCAAACAAACGCCAGTGACA
2807	ACGAATTGGGTAGCCGGA CTGAGA
2808	CTGTTCCAGTTCGGCAAGTGCGGC
2809	AGACAAGTCAGGAACGCGTTTCCG
2810	AGACGACGGCCAGATACGCTGCCA
2811	AGGAAGCGCTTCTTCCGGTTCTTC
2812	GATGGACGCAAACACAAGGCGATC
2813	CGCATAGCAGTCTCCGCATCTTGG
2814	TGGTTCGGGTGTGCAACAGATAAA
2815	CCGTATGCCACCTCCAGAACTCAA
2816	GTAAAGGAACCCCTCGGGAATCCT
2817	GCCTGATGCTCGTTAAAATTGCGT
2818	TCGCACTTGGACCATGAGATCTGA
2819	TTCTCAGGCTGGGCAAGAGTCTGT
2820	CGGACCTGGGGATGCTGGGATTAC
2821	TCGAGCCGATAGGGTTGGCATTGC
2822	TACGTGTGTCCACACACGTCGTA
2823	TGTGAAATTCGCGTTTCGCATCTT
2824	TTGCAATGCTCCAAAAAACTGCC
2825	TCTCATCATGGCTGTGGCTTTGAC
2826	ATTACACCGCTTGGTTTGGAGTGG

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2827	GCCGTGCAATGCACAGAGTTCAAG
2828	GAGATCAGACCGTGTCCGATGCTG
2829	CCACCTATCTTGATGCGACCTGGA
2830	CCGATCGCCGTTTATGTCTACGGC
2831	GAAAATCACGGTAAGGCACGTTCTG
2832	GATTCTCGCTTCCCAACGAGCATA
2833	CCAGAGCAGCATTCCACAATGGTG
2834	TGTGAAATGTGGCAGTCTCAGGGA
2835	CGATCCTGCGTGCCTCATCCAGGC
2836	CCCTCAAGTGGGCGAGGGTTTTCA
2837	TCGCCTCCGCCTCGTGTGTAGAAG
2838	TTCGCTTTCAGCTCATTGGAACGA
2839	TGTAATCTGAACAAGCGGACCCCT
2840	TGGAATCTTCTTGAGCGCCGTGA
2841	GGCTTTCATCTTTAACCGCTCGGT
2842	TGATCCGAGCCATTCTTAATCACC
2843	TGGTAGGCGTGATGTCCTACGCAA
2844	AGGCATCGGTAAGAAGGCCCTATG
2845	CGCCGCGAGACGATCCTTATTATT
2846	ACATGGACGAAATTACGCCCGTCA
2847	ACAGAAAGGTGGGGAGCCTAGCGT
2848	AGGCTTGCGAACATGGGTAGTGAC
2849	GCGTGGGCCTTGCTCCTGTTAAC
2850	GAATACAGAGCGTCCGATGTGCCC
2851	GCGACTCTGTAGGGAGCGCGATAT
2852	GGTGCACTCATATGCGTCGCATCG
2853	CTGTCCCACGGGGAAACCTTACTT
2854	TGGCTTACTGTCGCAATCTAGGCC
2855	GCACTCAGTTTCCGGTATCCCATG
2856	GTGAGGTTACGTAAGGCACAGCG
2857	GTAACGCCTTTGTCCCCAGCGTAT
2858	GCATTGATATGGTCGGTCTCGCCT
2859	GTGGGTTTAAGTGACAACGGACGC
2860	CAAAACCCTGCCGAAGATGTTGGT
2861	TCCGAGGAGACTGAACCTGCTACC
2862	CGGGGAAGAACGGATTGCTAAAT
2863	TGGTTAGCTTATGTCCGAGCCACC
2864	ACGCGTCGATGAACTAAGGCTCGC
2865	TTCTCCTGACGAGTACGCAGTGGG
2866	TCCGCGGTTGCCGGTTTGTTAGGA
2867	TGGCGCATCTTTCAGGGGATGATG
2868	TCTTTGGTCCTTGGTGTTTACGCG

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2869	GAGAACTCCCGCTACAAAGGAGCC
2870	TTAACGTGGGAACCGTTGGTGAAT
2871	GGGACACCATCCTTGGGTTTGTTA
2872	CAACAAACCGCCTTGGGAAGTGAC
2873	TTGAAGGCCACCGATACTGATCGC
2874	TCGTAATAGAACTGCGCCCAATGC
2875	GGCACGTTGCCCAAGTTGGATCCA
2876	ACATAGCTTGGCCGGACACCCACC
2877	CTTGCCGCCTTGCGAGTGGCTAAA
2878	AGTTCCGCGTCCTACTTCAACGCT
2879	AATGGCTCGCCAGATACCGCAGCC
2880	CAAAAGGCGTGTCCGAACTTTTC
2881	CGTCCACTTAGGTGGAGATACGCC
2882	GAGCCTCTTCGTCCTGAAGACCGA
2883	AACATCAAGCGGCAATCTCCCTTC
2884	CGTCCTGACATTATTAGCGCGTGC
2885	TGTGCAGACCCTAACGACCTACGG
2886	TTAGGTGGCCCTAGACCCTCCGTA
2887	TCACATCGCTTAACTGAGCGCATT
2888	AGACCTTCCCACGCGAGATGCTAC
2889	TTCTTGCCAAAATGTGTCCAACCA
2890	CAGTTTTTCATTGCAGCGAAAGCAA
2891	GTGCCGATCCCGAGACAAGTTCCG
2892	CATCCGGCCTCAGTGATTCTTACC
2893	TGCTGGAAGCCACAAACGTTACGT
2894	GAACGGCCAGGGGACAACATATCGT
2895	TCATCTAGGTCTGAAGCGCAAGACA
2896	TTTGGTTACCAGCACCCATGTTCC
2897	GACAACAGTCTGTCCGCCACATCC
2898	GCCAACAGGAGATGCTTGCACCAT
2899	CTAAGGACGCATTGACCCCTGAAC
2900	GGTCGCGTAGTGAGTCAGAGGCGT
2901	TTACCTCATGAACCTTCGCGGCG
2902	TATACAGCATCGTCGCCGGGCATA
2903	GCTTAGTGGCGTCTTCGTCGTAGG
2904	TGCACTCCGCAACCTTGTGAAATC
2905	AACCCGTCATGCCGACTCCATCTA
2906	AGCACTAGTGGCGTGCGACTTTGC
2907	TAAAAAGTGCCGCTAACCACGGAG
2908	CGCGGAATATTTGTCGTCCGATT
2909	TTCTGCTATGCGTATGGGGGCCCG
2910	CGAACTACTGCGTCAGCCTCTCCC

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2911	AGATGACGAATTAGCGGGGTTGGG
2912	AATAACAGTGGCAATGAGCGGGAA
2913	ATATGTTGATTCCCGTGCTGCACA
2914	AGAGTGGGCACCACCAGGCAGACA
2915	AGGCCTGGGTTTCTGCGTCTTAGT
2916	ATGACTTCAGGCACCTCAGCACCT
2917	CGGACGTGACAAACGGACATACCC
2918	CAAGTGTTCGGCCCAACTCTCGA
2919	GAACCCTTATCGGGATAGGCCCAA
2920	CAGGACGATACCAAGCAGAACGCC
2921	GCGTCTTGTGATTCTGCCCTAACC
2922	AAACAACCATCAATGTCGGGTCCA
2923	TGTAAAGACCAGTTGGCGGCTCTC
2924	GCGTTTTGACTCGGTGGTCAGTCC
2925	TGTATGGAGGCACGGCAAAGTCTT
2926	TTACCTAGGTTCCCGCTGACACGC
2927	CGGCTCGTGGGAATCCTCTGAAGA
2928	CCGGCTCGGGCATTCTTGACCT
2929	CAACGATGGAATTGTCTCCTTGGG
2930	CGGGCTATTATCGGGATTATGGGG
2931	ACGTACCTGAAGATGCAACGGCGG
2932	CATGGTGCAGCACGCACAAGTAAC
2933	CGTCGATATGTCGGGCTATTGCCT
2934	AAATGCAGGGTTAAGAGGAGGCC
2935	TGCAAGGACTGATTCTCCCGCTGT
2936	GTTTTCGGAACGCCGCAGAGTTCA
2937	CCCTCGATGGTTCATTGGGAAGAC
2938	CCTGTTGCTCATAATGGTGGGGT
2939	GAAAGAACGATCGCGGAATAGCTG
2940	TCCACCTGTGTGCCTTTATCCTCA
2941	TCCTCCGTGAACCGCTGTAGCGCA
2942	GCCCCAGAGAGTCCCTGCTCCCTA
2943	TTGAGATTTTACGGTTTCCCCGC
2944	CGATAGGACGTGGGCATGTCCCAG
2945	CCCGAACTTTGAGATCCGAGAACA
2946	TCACGCAGCTAGAGTCGCGTTACC
2947	AGATAACGCCCACTGACGACATGC
2948	ACGCTTAGAGCTCCGATGCCGAAT
2949	GGGCGATAACTTAAATTGTGCCGC
2950	AGGACGTTGATGCGTCTCTTGCA
2951	CGGCTGGTAGAACTGTGCATCGTA
2952	TTCGAAATGTAATTCCACGCGGA

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2953	GCAGGTTGGCTGTCTTGTGGAGTC
2954	CGTTTGGTTGCTTCAAGAACCGGT
2955	CATACTTGGTTGTTGTGCCACGC
2956	GGGGTCGGCTGAAGTGTTTTATCC
2957	GTGACGGTTGATTAACGACCGTGG
2958	CTTATGGCAGCGCCAGGGGCACTC
2959	GTTAGGGGACCCACCTCGTTTGAT
2960	CAATATAAATGCCGCGCATCGAGT
2961	TTCTTCATCAGCAGTCCCCGAGAA
2962	AGTTGCGTCCCTTGATGGCATTTT
2963	CCGACTTTCGTCCACGATTCTCT
2964	ACTTGCCGGACGACAGCAAAGAC
2965	CACCGCGGTAGATGTATCCCTTCC
2966	GTTAGCTTTAGCTCGGCACGCCTG
2967	GCGCATAAGAAGGTCCGCTAAAGC
2968	ACATCATCACGCCTGGCGTGACCA
2969	CCGGCGAAGTTTGGTGTGATTAGA
2970	TGGGAAGGCAACATGAAAGTCCTT
2971	TGCACCGCCAGATTGTGCTGAGTC
2972	ACATGTGAAGTGAGTGCCGTCCAA
2973	CCTCTGGAGGGGATTAGCCACGCT
2974	CAATAGCCATGTCACTGGCAACGG
2975	ACCCATGGTTCCAACGTTCTTTTCG
2976	AATCTGGTCTTGGCATCCTCCAAA
2977	GTATACCGGTGCATGCTGAAGCAA
2978	AGTGTTCTGGTTGAGTCGACCCG
2979	CGGGTATTCGACACACAGAGGAC
2980	AGTGCAACAGAGCGCTTGGTCACG
2981	TGCACCTATAGTTTGGTGCCGGTG
2982	TGCTCACGTACCAGGACACTCGAG
2983	AGTCCACACCTCGAACGACAGGCG
2984	CGCCGACCTGGTCAAAGAGCGCTA
2985	GCCTAAGGGCCTGTCGTTTTCCGA
2986	TGTGCGTGCTTATGTTCCGGTCTC
2987	CAACCGTTGGCCGTAACAAAATC
2988	CGAGAATCAAGGCGTACCATCTCG
2989	GCGTAGGCAGCCTCCAGGGAATGG
2990	GATGGTGTTTTCGCCAAGACCAAT
2991	CAAGCTAGGGACAGAATTGCCAC
2992	TAAATAGGCGAAACCGTTCGTGGC
2993	TCAAGACCCGCAATGTGTTTCATGT
2994	GCGGCTGGTAGACTCTTGCACAA

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2995	CAGGCGTAAACCTGAACCAAACGG
2996	GCCGATCTGTGCTGAGGTTTCATCA
2997	GATATCGCGTCGCAATATCACGCG
2998	CCCTGCACGATTAAGCCACCTGTA
2999	TGACATACAGATTTGTGTGGCCCC
3000	GTTTGCGGCCGGTATTCACGATGT
3001	TTTTACCTGGCCATTGGTGAGCTC
3002	CTCTACTCAATCAGGGTGGGAGCG
3003	GGGTTGGAGGGAGTCTTGACCATT
3004	CGAGGTCGGTAAGGAAAAGCTTGC
3005	CTTTACGCAGGCACCTCCGAGCTG
3006	CATTGTATGGCCACGTGATTGACG
3007	GTACGGTGCAGAGAGCGCCTAAGCG
3008	TTCCATATGCCGAAATGGACACAA
3009	TACGCCTTCCGCTATAGCTCGTGA
3010	CTGGCCGCTCGGCTAGCCATCAAT
3011	CTGTACGCCACGCATGAAGGGTGA
3012	CTTACGCGTCCAATGACTGCCACC
3013	CACATGGTAGAACTCGATCGGCAG
3014	CGCACCGGAAACTAGTGGATGTGT
3015	ACTATGGCAACCGACACTTGGTCC
3016	CTAGTTTGCGCTACCCACCTGCAA
3017	TAGTATCGCCCCACAATAGCCTGG
3018	CCAATATTTACGGCCTGATCAGCG
3019	ATGGCTATCCCTTACTGGCTCGCC
3020	CAAAACTTGGCAGGCTTGGGACTT
3021	AATGACCGAGGCTGCAAGATTGAC
3022	ATCATCTTTCGCCACCAGACATGG
3023	CGTTATTACCGATGCACACGTTGC
3024	CACACTGGCAATCGCCTCCCTCGT
3025	AGGTTGGTAGGAAATCGGAGCGCT
3026	GCTGAACCACTGTGGTCAAGATGC
3027	CGTTGAGTACGACACGGTCGAGGT
3028	TTTTTCCGCCGCAATGTGATCTAA
3029	ACAATACCTCGACCGCTCAGCATC
3030	AGTATCCCTGCTGGCATACACGGG
3031	TCTTGGGCTCGGTAGTTCAGCACT
3032	CCCTATATCGAGCCCATAGGGCGA
3033	CACGAGTGGCATCAACGGCCTACT
3034	TGCAGGGTCCGATGTGTTCAAGTA
3035	GCTTGACCGCTGCTAACCTCGTAC
3036	TTTTGCATCTCTCCACCATCCAGA



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3037	AGAATGTGCACCGGCTTCCATCTT
3038	TGTTATGACCCGCTCTGTGGCGTG
3039	GGAGCTCCTGTTTCATCGAGGCTA
3040	CATTTTGCTGTTTGGGGTCCCAT
3041	CCCCTCCTTCACGTGAGACGAGA
3042	GCGCTCAAGTCGATTGCCACAACC
3043	CGGTTGACGGAGACCGCAGTACTT
3044	ACTCAAGACCGGTGCACCTCCAGC
3045	TGGATGTCGAGCGTGTCTGAGTTT
3046	TTTCGTGTGCATGCAAGTAATGGC
3047	GCGGCGTTAGCTCGAGCTAACAAA
3048	GGGTATCCTGCCCCGAGCAGTAATT
3049	GGCTCCGAATCTCTTGTCCGGTCT
3050	AGGATGGCCACGCCGAATCAAAGT
3051	GTGCGGGGACGTTTACATAACGAG
3052	ACTTTTGACCTGAGGCCGCTTGCA
3053	ACTCCGCTTCAATGGAGACCGTTG
3054	GATCGGAATTCGCCGCCATATTGA
3055	ATGCGTGCCCATGGAATGACTTTT
3056	CCGCATCGCACGAAGGCAGGTCAT
3057	CACCCTATGCGTCTCCAATTCCTG
3058	TGATATGCATCGCTGAGCCTCTGT
3059	AGCTTCACACGCTCACTGAACCTG
3060	AACCCGGAACCTCCTCTCACTCGG
3061	CTCGTCAAACCTTGCCCGAGGAGTC
3062	GTAGCTGGCAACAGGCAATCAGGA
3063	CTTGTCACGAATATTCGCCAAGCG
3064	CAGTATCTGAAACACGGGGTGCTG
3065	GGCTAAAATGGGCGCCACGTGTA
3066	ATGAGAGCCAAGCGCCTCAACTCC
3067	TATTGTTAGGCACCGCTTCGCGCT
3068	GGAAGTAGATTGCCAGTGCTCGCC
3069	AGTCGACCCCAAGGCAACTGGGTC
3070	GGTACTGTTAGCTCGACGATGGCC
3071	CCGCAATACTTGACGGTAACAGGG
3072	AATTCCGGGTTTGAACGGTTGGAA
3073	GACACGCAATCGGGTCTATGCGAA
3074	GATTTTGGCGTCTCATTGCGTGAT
3075	TGCCATAGGGAGGAAACGCAATTA
3076	GAGGTGCCCATGTTAGTGGTGTCC
3077	GCTTTAGCGGTCATACGACCACCA
3078	CCGCTACCAACAATCCGATTAACG

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3079	CATAGTGGGCTGAAACCCCAGGAA
3080	GAGGATCTGGCCACATCGAGAAAG
3081	CTCGTTTGGTACCACGTTTTGCCG
3082	AATACACGCGGCGTAAACAGACGA
3083	TGTCATGGGCCAAATGACAGTGGC
3084	ACAGCACTCCGACCCGTGTACGA
3085	CTCCGTAAAGAGCACAGCTTTGCC
3086	ACGAACAGGTAGGGATCGGTCCTC
3087	TGGATCCACCTTACCGCGCCATCG
3088	AGTATCAAATAGCGGCGCGGCAAG
3089	GAATTACATTGTGGATGGAGGCGG
3090	CTCCTCGGGGAGTCGAGGAGTACG
3091	AGTGTCGAGCCAACTCCCACCAAT
3092	AAATGACATCCGTTTGGCCACAGC
3093	CGAATCATATCGCCATCGAACTGG
3094	TATAATGCACTCGCTTGGTGCGCA
3095	GCCAAGCAGATGGTAATTATGGCG
3096	CACGCGGAAGAGCACGTAGAACT
3097	TACCCGAGAATTTGGAGAACAGCG
3098	TGACGGCAAACGTGGCATCTATC
3099	CACAGTGTTCCAGCCCTTGACGAT
3100	TACCCGCCCACACATGAAAGTTGG
3101	TGGCATATTTAAGATTGGCGACG
3102	ACTGAAAAAAGAACGGGTAGCGGG
3103	TCTGACCGCAATAGGTGGTCATTG
3104	ACTTTTTGGCGGGCCCTCTCTCGT
3105	CTGCCCAGATCATTGCGCGATCCG
3106	CGGAGGTTAAATGCTTTAACCGGC
3107	AGGCGTCTCCAAACGTCCTTCTGT
3108	AGATGCTATCCTGAGTGGGCCTGC
3109	ACAGGGTGAAGAGACCGTGGGATG
3110	GACTGTCTAACGGACGACACGACG
3111	AGCTGTTAGGACCCGACAACCGGT
3112	TTGCGTAGTGTGGGCATTTCTCT
3113	ATGCGCGCTTCTTTCTTGATGTA
3114	TTAAGGGCGTCCGCGTCTATTAG
3115	ACCTTTAACTTGTACCGCGGCCC
3116	AGGGATGCAGAGGCACCACATGTT
3117	CGGTTGACGTATGAGCATCCGCA
3118	CAGGGCGATAGTCACATGGAGGTT
3119	GCTTGACTGCCCCGTTTCATATGT
3120	CGAAGGGGTTGTGCAATTACCCGA

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3121	AAAACGCACCGCAATGACAAAATT
3122	ATTCCTGGACAAGACCCTCAACCG
3123	CCTACCTGCCTGCTAGCGGTGAGG
3124	GCTCGTAAATGGGGAGGAATTGGA
3125	ACATGAAAACAGGCTCAATTGGGG
3126	GTTCCGCACATGGATTGAGGTCTC
3127	GGCACCCAATACCACGAAGAAGAA
3128	AGGGGCATTTTGAAGTCCATCTTT
3129	CATCATCACAAAGGAACGTCGGTG
3130	TAAAGACCCACCGTCAGCAGCAGC
3131	CCCCAGGCGTAATGCACCACATAG
3132	GCAGGTGGAACGCTAGTGGTTGAA
3133	GGAAGTTAGGAGTTCACGTCGCCA
3134	GCAGATACGGCTAGCTGAGGTGGC
3135	CACAGGCCTAGAGCCTCGGCGTTC
3136	GTTTTGCGCGCATGAGGTTCTTA
3137	TTGCGCCTGATGCCAGCAGTACTA
3138	GATATCAGGCTTTCCCACTGCCGC
3139	TGCGCGGAGACGGAGATCTATGAA
3140	CATTGGTGTGGCTGAGAGTGGAC
3141	GTCGGCACTTGGGCACCATTAAATA
3142	ATCGATCGGTGTCTCACCACGGAG
3143	CGTAGCCTTCCACCGTGTGATAG
3144	CGCTCTCCGTCTGAGGAAAAGGGG
3145	TCGCCCCAGCCAAGGATATATTGC
3146	TCTCTTGCAAGGAACTCTGCCGTC
3147	GTCCTGGACAGACGGAGGGTGTTA
3148	GCCAAATTAAGCGGGCTCGTAATC
3149	CCATTTGTTGACCGATGGGAGGGG
3150	TGGTCAAAAGAGCACGATCCAGGA
3151	CGCTACTAAGACGCCCCTGTCCAC
3152	CATACCTCCCGCTTGATTCACTG
3153	CCGCGGAAGGAATGTCATCTACAA
3154	CACGGGACATTCATTACAGGACG
3155	ACTAGTGAGGCGTGAGGCGGGCGT
3156	AGGAGTCACCCACTCCGCACAAAA
3157	TCATGACAGCGCACCCCATACCAT
3158	GGTAGGGGACTATCGATCGTGCTG
3159	ATGTCTCACTACCGCACGTAGCGG
3160	TACTGCTCCGGTCTTCCGCAGCTT
3161	ACGGAGGAGCGACTCGTTCGCTGC
3162	GAAGTCTGTCGCCGGTGGACGGAC

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3163	CCGTAACGTGTATTCCGACGAGCG
3164	CGTGGAAGCGACTTAACCAATCGT
3165	GGCATGGGCTATGCCTCACACTAG
3166	GGGTCGTATTTAGCATCGTTCGT
3167	AATGGTCGCGCAAACCGTAAGAAT
3168	CTGGATTCCGGTACGTCCAACGTTT
3169	CGCAAAAACACCCGTAGCCAAGAA
3170	TATGGATACGCTTTTGGACTGGGC
3171	GCTTCAAACGCGCTTCACGCTGGT
3172	TACAGCCCGCTCTACCTCGCCACC
3173	TCAACCGATGTCAAATGCACGTT
3174	AGCTCTCTCCGAAGTAGGGCGGTA
3175	ACGCACACATGGAGACTTGGCTCC
3176	TTCTTGAAAGCTAGTGGGGCGCTA
3177	CAATCACGGCTGGGCTATTCTGTG
3178	GTGGCGACCCGTCGGTGAAAGAGT
3179	CGTCGAATGCCGAACCAAGTTAAGT
3180	TGCGTATTTGCATGCTCACAGCTG
3181	CGCAGTTGGTTGTGCACGGCTGC
3182	GTTTTTCCGTGAAAAGTGGCATCG
3183	ACAGGTTCTCCACCACGATTTGA
3184	CTAGCGCGCTTTTAGGTCCTTGCG
3185	CAAAATCAAAGGGATCAACCGGTG
3186	AACGTAACCCCAAGTGAATCAGGCA
3187	TCAACCGGTGCACTTTAGAAGGCC
3188	ATCGCAAAGTTGCAGGCGAATACT
3189	ATATGTCCCTGGGTGCTGCACAAC
3190	TGGCACTTTGTAGTGCTGCGGTGG
3191	ACGCACGACGTCCTTCTAAGCTCG
3192	CCCACGTGCACTATAGGGATTTCTG
3193	CCGCGCTTGGTCAGTCATCCTTGC
3194	AGCGGCTCAGGGAATAACAACAGG
3195	ACAACGCGATCGGAGGCAACCACT
3196	AGCAATTGCCTCCGTAGAAACCCA
3197	GAGTCGTGGCATCGCCTGCTATCG
3198	TCTATGCAAATACTGCGCTTGCGA
3199	TCAGCTTAAGTTACGGTGTGGCCG
3200	TCCAAGGTCGAACAGGGATCAGAA
3201	GTTAGGCTGGCGTCAATAGCGCTT
3202	GGTGTGATAAGGAAGAGGGCATCG
3203	CCGGCGGGCTAGATCAATATTTCT
3204	CTAACGTCAAGTTTACGCCCCGA

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3205	GCAGCACAGTTTTCCGATTGCGG
3206	CGCACGCAAGGGGAGGGATGACTG
3207	CGGGGCCGAAAAGGACGTCACAAG
3208	TTCTCCAACACGGCTAACCGGTAG
3209	TTACAGCCTGGCCCGAGGTAGTTG
3210	TTTCGGGCAGCATGAGTTATCGAA
3211	CTACTGGACGCCCTGCTTCGAAGT
3212	GGTCGTCCGACGTGAAAAGACCAA
3213	GTTTTCGAGCTCTTCTCCGCAGG
3214	GCGTGAAGGTACCCAGTGTCACAG
3215	TTTCTGAACGCTTCGACGCAACAC
3216	TGCTAATAAGCACGCCTAGCCCGT
3217	AAATTAATTGTGGTGGCTCCGGCG
3218	TTACAATCCTCGGGCTCACTGACA
3219	GCTGAAGGACAAGGCGTGGGCAAC
3220	GGGATAGGAGACCCTCGCAATGGT
3221	TTGCAGTACGTCCTTGCGCATGAA
3222	TTGATCACTGGATTGGGTGCGAAC
3223	TCTGCAGACGTTGCGAGAGATGAT
3224	AGTCTAGCAGGGATCGAAGCGGAT
3225	GGGGTCCCGCAACAATAATGAAG
3226	CAACCTCTTATGTGGTGTGCGCGA
3227	CTCGCTGGGTGCTGGAGTAGCAC
3228	CGTTGTATTGTGCAACGCGAAGTT
3229	GGGCTCAAAGTGCCTGAGTCGAAA
3230	CTGCTGTGCCCTCTCAGTGAGAGC
3231	CGGACGTA CTGTTCCGAGTCCTCA
3232	GTATACCACCATAACCGGGACCGCA
3233	CTGCTGCGAAGGGAGACACGTCCG
3234	AAAGAACGTGGAGGATCCATTGGG
3235	TCGATTGGCTGATCTCCAGCCTAC
3236	CTGCGAATTCGAAGGTTGTTACGG
3237	GCAGGAGGGTCAGGAGTACGTGAG
3238	ACCAACGGAAGGGAACCTTAAGGGC
3239	ATGATGGAGGCTGCGTTTTGGTCG
3240	AAGCCCAATTTACCGCTCCGAATA
3241	CTAGGCTGTGCGGGACTAGAGGTG
3242	TGCCATCTGACCTGGTGATTGCGT
3243	GTCGTCAACTTTTATCGCGCACCT
3244	TTGAATGTAGGCTGCTGCAAGCGC
3245	CACCTATCGTGGCCTCTGTCCCAG
3246	GGAGCGCCAGTATAATGAACGTG

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3247	AATGGGGGTTCTTAGGGTGCCGTA
3248	GCCATGAGGAAAAGCACTGGGTCT
3249	TCCGGGTCGTACTGTGTATGATCG
3250	GGAGGTTATGTGCTGCTGATGACG
3251	CTTCAGCCGTGAATGGTGTGAAAG
3252	CTTCAAGGGCTTCGTCTGCTCGTG
3253	TCAGGGGTCACGCATTGGGTTTCA
3254	ACGGTCCTCGCATAATGGACCACT
3255	AGGCGTAAACGCCGGTCATAGTCT
3256	GATCTGGTCGGAAAACAGGAGCGC
3257	CCCATCGATGTTATTTCCGACGCA
3258	TGTTTCTCCGCATCAGTACCGCAT
3259	CGGACCCGGATCGACAAGTAGTCA
3260	AGCCAGAGCATGAACTGGAGCGTC
3261	TGGAGTTTACATCGGAACGCAGGG
3262	TCGACCACCGGTACGATACAATCA
3263	GCTTGTGGAATTCCGACGGTTCCA
3264	CACATCCACCCTACTGAGGCACAA
3265	GCCGGATGAATCTGCCTCGCTACA
3266	GGTTGCAATTACGCCGGGATTAAA
3267	ATTTCTCGCAAATCGTCTGGGTG
3268	GCTCCTACGCCATGTGCACGTTTA
3269	AGGGTTGTCGAAACATGGGGGTGA
3270	ACGCGACCTGCTGTCAGCGTGGTG
3271	CGCCTAACTAGGGGAGTGAACGGA
3272	GTTGACCTCCGGATTGCTCACGA
3273	TACCTCCGTCACTCACTCTTCCCG
3274	GGCGTTCCACATGTAATTGGGTCT
3275	CGCATCACGATCGTTAGGAGGGAG
3276	GGGCATTAAGCACGCACTTCGTCA
3277	TTTCATAATTCGACACCACGCGG
3278	GACCATGAGATGCTTTTCTTGCGC
3279	CGCGGTCGTCCTCAGAGAATGTTG
3280	TGCTGTGACGATGGCTCCTACCCG
3281	GGCGAATGCTTCTTCGCATCAAGT
3282	AAATGCACAGCGGAACTGACCACA
3283	TATCGACCTGGAACACGATCGGTT
3284	CATTGAAGTCATGAAGCCTGGTGG
3285	CTTTCAACCGTAGTGGCTTGGGCA
3286	CCGGAAGGTCTGAATTGGAGCCTA
3287	GGATTGAAAAATCGCCGGAAGATC
3288	TGAAATTGTGAGGGAGCCTTAGCG

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3289	AGCGGGATCCCAGAGTTTCGAAAA
3290	CGAGTGTCACCTGGTCGGTTGCTCA
3291	GCAGCATCCGTTCCCCTATAGTGG
3292	GTATTCCTGACCGGCTGAGTGTCG
3293	GCAGCGTATGGGGTTAGCCAATGA
3294	CGCCCTGGTGGAGTTGTATGATGA
3295	AGGTAGACTGCCCCGCGGCAGAGCA
3296	ATGCGTGAGGAACTGACTTCGGAC
3297	ACGGGAGAGGACATGCATTTTCAA
3298	ATTCATGCAGGAAGTCCGAGGGAA
3299	AGCTCTCTCCGAAGTAGGGCGGTA
3300	TGGCCACATGATTGGAGCTCCAA
3301	GCCCTTTGCTTGCATTGATTGATC
3302	AGGAGATTCTTCGGCTCATCTCGC
3303	GCAGCTCCGCCAACGAACTTATAG
3304	TGGGTCAGCTTCGGCCAGGCTGAT
3305	ACGCTCAGCGTGCGCTAGATACGA
3306	GCAACGAGAGCGAACGGTTAACTC
3307	GAACACAAACAGAGGTCGTCAGCG
3308	CGTGCGTTAGCGTCGGCGTATGTT
3309	GTGCTAGCCGAAAGTAGCGTGCGA
3310	CGCGGAGGTTTGCAAGTTGTTAAC
3311	TACTGCCCCGCCCTGAAATGACTTA
3312	CATGCGCACATGAGGGTCACCTTT
3313	CTCGGGTTCTGAAAGCGATGCTTC
3314	GGCACACAACGAAGGCTGATGATA
3315	GGAGGCCGAGTAACCTTGAGGGTC
3316	ATTCCTATCGCGCGTGCTTCTAGC
3317	TTGCCGGTGTGTTCTGTGAGCTGTT
3318	TTATGGGAATCTACAAAGGGCCGG
3319	GGGTGATCCAAAATCCACGAGGC
3320	GCGAGATGAGCAAATTGTATCCCG
3321	CCTGCACACATCATGTCTCAATGC
3322	GGCAGCGTAGGGATTTCTAGGGG
3323	AGAGATTGCTCCTATGTCGGCAGC
3324	CCAATACCCTGGTGACCACTCCAA
3325	GACGTCTGTTATGTCGTCGCAAGG
3326	CCACAACGTCGAAATGACCTACCA
3327	CTTGGTGGCATGCATGCCTTGCCC
3328	TACGTTGCCCCGACGTGGAATAAA
3329	GGAAGAGAAAACCGACAGTCGCGA
3330	GACGAACAAGAATTTGGGGCAACC

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3331	CGTGCCCGCGAGTTCATGGTGCTA
3332	AAGAGAAACCCTTTCCGGAGCTCA
3333	TTTTAAATCTGCCGCCCTTCCATG
3334	TCTGAAGCAATTTGGCCTCCTCAA
3335	GATGCGCAAGAGGGTATTATGGGC
3336	GTGAAAATCTCGCAACTTCCTGGC
3337	ACGGGAAGCGGTGAATTGTTGGTA
3338	GCCCTACTATTGCCTTGGCAATGA
3339	GTAAATGGCAGGAAGCGGCTCTCG
3340	AGGTGCCAAATAGTGGAAGTGGGT
3341	TCGGATGGTAGGAGGCGAGATCGG
3342	GAGGTGAAGGAACAGCGACGCTAA
3343	ACCGTCGTTACCGCTCTGGTGTCTG
3344	TTCCAATGTCCGACATGCTATGCC
3345	CGGCTTTATAGGTCCAACATGGCG
3346	CCGGCCTGGAAAGCAGAGTTATTG
3347	TTTATCGTTCAACGCTCACGTCCC
3348	AGACCCGCTGAACGGAGCTTGGAT
3349	ATCCATCAGGAGAAAGCTGGCTCA
3350	TTGCCAATGCGTAAATCGGTTCTC
3351	GCTTGGCAGAAGGCGTACACTAGG
3352	AGGCTCCAATGCTTTAGCCGCAA
3353	GATACTAGGAGCGAGCCCCCTTGG
3354	GTCGTGTGCAGCCGCATATGGAGG
3355	TACCCCTGTTGCGGATAGATGTCTG
3356	TAGGGTAACAGAATGAGGGGCGCT
3357	ATCGTGTGCGGGATCGAATTTGAG
3358	ATCTCTCGTGCGGTCTTGCAGAAG
3359	AGAAGCCACATGTTAGTGCGGGAG
3360	ATCTGCGTTAACTGTCCCGACTGG
3361	CGCTCACAACGAGCTTACTCATGG
3362	TCTACGCTACGATCCGTTGCATCA
3363	TTTAACACCGAAATGGGAGCGTCC
3364	ACAGGGCGTAGTAGGCCGCTTTCC
3365	GTCGACCGTGTTTGTGGGGGATAT
3366	AGAAGACCTTGGCAATCCGAGTCA
3367	TTGGGTGCTTAAAATGCGGTCTGA
3368	AGCGAAGTCGTATTGACGTGCGGT
3369	ACTTTCAGCTCCCAGTAGCACGCA
3370	GCGCATGGTGAGTCCGTATTGCCG
3371	GGGTCGTGTGAGAGGACAAACACC
3372	ACAAGAGGACCTCCGGGTGAAAAT



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3373	TAGCGGGGACCTATCCGCCTCAGT
3374	GCTCTATGCCATGTCCGTGGATTC
3375	AGCTCATAATGCGCGTTGACCCCG
3376	ACAGTGGAACGTTTCATGCCGAG
3377	GGTTTCGACGAAAAGGATGGTCGT
3378	GCGGTACGTATTCTAACCCGACGG
3379	GGTATTCGCCATGCTTGGTCTCTG
3380	GAGCCTCTCCGATTCTGGCCCAGA
3381	TGGAACGTAATACGAACGCCGAAC
3382	GGCAGAAGTGGAAGTGAAGCTCGAT
3383	CGGGTAGGCCTTCAGGGTACAGGT
3384	AGCGATCTTGGACGCCGGCACGAT
3385	GACCAGGTTGGTACAACGCCTTGG
3386	GATGTGCTACAGGACCGCCTACGC
3387	TGAGGCGCACTCATTAGGAGGTGT
3388	CACCTTACATCCCGAATCCGCGTA
3389	CCAAACATAAGGTGTGTCGGTCCA
3390	GCGTTTGCTAATGGTTGCGATTGC
3391	CCCTTGCCCTCAATCTGTATTGCA
3392	ATAGTCCCGTGCGACTGTGATCC
3393	GAAGTTCCCGGCCCGAGTAACATA
3394	GGGAGCCACGACAGAGCTCCTAGG
3395	CTGACTCTTACGAAGCGCACTCGC
3396	AGGTATAGCGGGGCGTCTAGCAAA
3397	TAAGACGCATTGCTTGGACCATCC
3398	GCCTAGTAGGCCACGGCTTCATGC
3399	CGTGCCCTAGCATACAACGTTGGG
3400	GGGAATGCGGCAGTCTGTCTACCT
3401	GTTGAAATACTGGCCCCGCGGGAC
3402	CGGACAGGTGAACCCAGTCACCTT
3403	CAACAGCCCCGCTCCTTGGATATAA
3404	TTAAAGGAATCAGGGGGACCCGCC
3405	CGGGTTGTAACGCTGTTGGACGAA
3406	GGTACGCAGCGGGACCAATAGAAA
3407	ACTGCAAGCCTCTTAGTTCCTGCG
3408	TCAATACCACCCAGAACTGGGCG
3409	GGCAGTTGACACTCATCGACCATC
3410	TAGCACGGCCATAAGACGTTGAA
3411	TCCACAATGTCAGCTCACTGCAAA
3412	CAGGCGGAGGGGTTTACATCCTA
3413	AGGGCACTCGAAGATCCGACGGGC
3414	CGCAATGCCTTTTGCTGTGGTAAT

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3415	AGAAACGCAGACGTGGCGTTTTGT
3416	TGAGCACGAATGTCGAACAGTCAA
3417	CTCGTTTCCATGGGGTAACCGACT
3418	CCTCATAGCTACGGGTGGACGACG
3419	GTACGCCGTGTATCACCCATTCA
3420	ACCCATAGTTCGTGATAGCGCGA
3421	TCTGCAGTGTTGCCCTCCGACGC
3422	TGCACATGCAACTAATAGGTGCGC
3423	CAGCGCAGTGCCTTACCAATATGA
3424	TTACGCGCCGAAAACACCTGAACA
3425	CTCCCTCGCTTTATATAGGCGGCG
3426	GTCGGACCCCGAGAGTCCTGTAA
3427	ATCGACGAACAGGGCCTCCGGCTT
3428	TGGTTTTTCACCTCCGTCTCAAG
3429	GGAGGGGGCCAACTCCTTGACTTG
3430	TCCTGTCTCGGCCTTTGGGAACTT
3431	CAAGCCATTACCCGCTAGCTGAAA
3432	CGCAACCGACATTATATTTGCGCC
3433	TTGAGGGCGACTGCAACACACAGG
3434	GCTCGAGTAACACGGTTGACCCGA
3435	CAGCCCTAGCGCCACGGTAAAATC
3436	GTCATTAGCGACTTACCCGCCGTA
3437	CCCAGTGCCCGGCCCTAGATAATA
3438	CATTCCGTATGCTACTCGCGAACA
3439	AAGTTTTAACGCTCAAGGGGGCCT
3440	TTGGCGGTTTCGGTACAGGATCCT
3441	TACTGCGATGATGGGGATTGACA
3442	CGGTGAGCGAAGATCATCCCCTTA
3443	ATGCAAGTCACCGACCGGCACCTC
3444	CAAGTGCCGCAATTGGCCTTTTAT
3445	CCCGTGGTGGATACCTGGGTAAGC
3446	CCGTCAGGGTCTAAGGACCAGGGT
3447	CTTTCCGTAGGCGGTGATTTCCAA
3448	GCTGAAACTGAGATGGTATCCGGC
3449	CCAACGAGACAGCATGAAGCTCCT
3450	ATAAGTTCGTGGGCCGGAAGGTC
3451	GTGGCCAGGCCATAACTGGTCACT
3452	CGCTTAGCGCGAGACTCTGAGGGC
3453	AAGAGCGCGCCCTAGAACCCAAC
3454	CCACGGGAACGTCTACGAAATGAT
3455	AGTCGTGTATCAGGTGCCGAGAGG
3456	TGAAGCGGCTGGCGATAAGTAGAT

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3457	CTGAGGACGTGCGGTTTCATGCTGA
3458	GAAGGCGTTCGGAAAGTTTTTCGT
3459	AAGAAAACCACGGCTGAGACCTGA
3460	TCAGCCGCTGTTGCAGGGAGAAAA
3461	TTCTGGAAATGGATCGGATAGGCA
3462	GGGAAATGGTCTTGTGGCGACCA
3463	GGTGTGGAAGCCACGATGTATCCC
3464	CCCCGACTCCCTTCGGGCATAAGT
3465	CCAAATGCGATAACGCAGCGTGAT
3466	GCTCGCCAACGTACGAGGCTCAGA
3467	GGCTTATCAGTCGCCACCAGAGAC
3468	GATGTGACCCATCCATTCTGGGA
3469	TCCTGGTTTGGTATCCCCGAATCA
3470	CGCCCCGTATATAGCCGGTAAGAG
3471	GGTTCACTGTAACGATCGCGGCAC
3472	CCGGTATAGAGGAAACCCGGACGT
3473	CCTCCCAGGAGATCCTACGCAATT
3474	TGAAACTCGTCACGCTCCTTGCA
3475	TGTTGCGTAACCACCAACCCTCCT
3476	GCAGCGCAACCTTGACTTCTTGC
3477	CGCAAGTGGGAGCCCAAGAGTTTG
3478	TGCAGGGTAACGAGGGTAAGTGGG
3479	GAAGTGTAGGGTCTCGCCGGTCAA
3480	CGAGATGTCCAGCAGCGGTTGTTA
3481	TTGTGGTTGCTCCGGGTAAAAGGA
3482	TCTACGCATCCCTGGGTAATTTGC
3483	AGAAGCTGCGAGTCACCGTGA
3484	GGGCGGTGTTGAAGGGCTCTATAC
3485	TTCCACAACGGGTGAGTAGGACGG
3486	GCAGCCAGACTGGCCTACCGATCG
3487	CCCGCCGAGTTGGTTGGCTAAACA
3488	GCTAGGGTGGTCCTTTCA
3489	CGTGA
3490	ACTGCCCATGGGCCACTAGGCTTG
3491	GGCGTACGAAAAGGCCAATCACTT
3492	ACTTGTGGTCGACAACGATGTGGC
3493	CCACCACCCCTGACCCGAAAAAAT
3494	TGTTGTGCATCACAAATCAGGCC
3495	GACCACCCGGTAAAGAGGGATGGT
3496	GCCACCCCTGAAGCACTCGTTATG
3497	GCTACCAAGTTGGAAGACGGGTTGC
3498	CAACGTTTCGCATCCCACAGTTGTA

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3499	TATCGGGTCGTAATGGGCAAAGAG
3500	TCGGTGTGATTGATGGATAACGCC
3501	AGAGGTCGAGAGCCCGATAACCTG
3502	GTAGTTAGGCGCGGCCCTGGCTCA
3503	TGATTCTCGATGTCACGCCGAACA
3504	GATGGTTCGCCCTTGTGTCGCAGC
3505	GCGCAGTTACGTCCATTGTCCAC
3506	CCGCCTGATTTAACAAGCCAAGGT
3507	GACCAAGTGCAGGCGTCAGTCTGG
3508	CAAAAAGCAATTCGCCCTGGACG
3509	ACTGACCTTCTCGCTCTCTCCGTG
3510	CTCGCCGTGATCGCTAACCTCT
3511	CGGCATTTTTCACATGCTGTGTTG
3512	ACGTAACGCCTGATGGGGTACACC
3513	CCCTGTGACCGTGGGAGACACACA
3514	GCGCATACTCTGGGTAGTCGGCAC
3515	TCCCCTGCCCATCTCTGAGTTAGG
3516	TGCAGCGCTAACATAGCGGGTGCA
3517	GCAGCGTCCACAGGAAACCGCAGC
3518	AGCGTACCATCGATGGGGATTCTGA
3519	TGGCCTCGCGATCACCACGATGTT
3520	TTGGTAATCACTCGGCCAGCGCTA
3521	CGTTAGTAACGATCGTCGGTGCAA
3522	AATCGCAGATGGTTCGTGGCACAA
3523	TAAAGCGTCTAGAGGCCGGCTGTG
3524	TGGCTAAACGAACTGGGAATCGG
3525	CCTATGCAGCCACTGGTGTCTTC
3526	ACGTGAGATCCAAGGGTGGCTCCT
3527	TAAACGCCAAAAACCACGAGCAGG
3528	CCATGGAATGGAAGCATTGGACG
3529	ATGATCCCTGGGCTTAGTCGCCTT
3530	ACCGTATGCCTCAACAGAGTGGCT
3531	CCACCAAATCGCATAAGCTCCACC
3532	TCTCAGTTTAATCCCGTGATCGGG
3533	AAAGGACTACGCCCATCGCTCACA
3534	CGGGAAGAAAGGCCTAAAGCTTTG
3535	TTTTGGACATTTTCTGCATCGGG
3536	GCAGGGGTCTTTTCCACGGTAAT
3537	TCAATAGGGCGTAGGCAAGCTTG
3538	ATGAAGTTCCATCCTGTCCGGGCC
3539	AGAATGATTAAGCGCAAACGCAGC
3540	GGCAGCAGAGAGTGGCCTAGTTCC

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3541	GTGCAGAGCCGGCCTTATGTAAGA
3542	CATACGGGTATGGCGATGGTTACC
3543	AAGAACAGGAACCGCTGACAAGGA
3544	GATGTGTGTCGCGTCCTTAAGGGC
3545	TATCCATGTAAGGCTCCTGAGGCG
3546	AGTTTTTTCCTAAACGATCCGCGC
3547	CTGACCGGACGACCCAGAATGTAT
3548	GCATGTGGTCAAAGCTTGTGATG
3549	CAGAAGTGCATGGGTTGCGATGAA
3550	ATAGCGTACCGGAGGGCTTACCAG
3551	AAGACTTGGCGCTTGTGGGTAAGG
3552	TATTGTGGCGCCTCACGCGCAATC
3553	TCGGCCATGGGATTTACAAAGTC
3554	TGGTCGGTGCCGTTTCACCTTTAC
3555	CATTTCCGCGGGCAGGAGAAAGAT
3556	CCTGAGTCGCGATACGACTCAACA
3557	AGGTGTACCGCCGTCGGGTTATAC
3558	TCCTTGTACGAGCCAAGCCTGGGT
3559	AGAAGCCCGAAGTCCCGTGTAGAC
3560	AGAGGGGCCCTTAGGCAAATACGT
3561	ATGCGGCAACATCCGATCGTAGAT
3562	CGCAGTGGGCAGTAAAGACAGAGG
3563	TCGGGTAGTGCAAACCTCAATCGT
3564	TCTTCACTGTGGTGGACTTGGGG
3565	GTCCCAGGGCGATTGGTACTAAGG
3566	GGTAGATCCAGCCATTGGGACCTC
3567	GGGGATTGTGCGCTCCAAGGACCC
3568	CTCTGTCCTAGACTGAGCCGTCGC
3569	CGATGAACAAATGAGTGCGTGTGA
3570	GAGGTGAGCTGCCTGAGAGGAGT
3571	CAGTGGGACTGCTAACGTGGGTCA
3572	GAGTCGCTCGAGGAACACGGCCG
3573	CGGCTACGGAATGATGCAGGATGG
3574	TCGCTCTCGCTATGGCAATTCTGG
3575	TGAATCACGGCCCTCTCTGGTACA
3576	CAGGTGCCATCGAGCGCTTTAGTG
3577	TGGGAAAATCGAAATCGTCAGGAA
3578	CGGGGAGGAAGATGTTCCAGCGGT
3579	TGTGGACCGGTGGTCACGTCTTTT
3580	GCACGTCTCGCAATCTGCGATCAG
3581	CCTAATGCCGTATCAGCGACCAGA
3582	ATAACGCGGGTGAAGGATTTCGTCT

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3583	TTCAACCTTGTGGGGCGTCCCACT
3584	CTACTTCCAAATCTCCGCGTCGGT
3585	AGCGAACGCACTGCCAGTGGATAC
3586	GAAAGTGGCGGCGAGGAAAAACAC
3587	CAGGGGGCGCATATTTGACAGATT
3588	TAACGCTGCCCTCAACTCAGGG
3589	TCGATTGTTGGGTCTACCGTGGTT
3590	GCTGGGATTAGTGCCGGGTAACCG
3591	TGGTTGCAACATCGCGCTATTACG
3592	GGGCGTGCTTTGAGCTGAAGCGTG
3593	ATGTTGAGGTTAGTCCCCGACCGT
3594	GACCGCGTAGTTAGCAATGTTGCG
3595	CCAACCCACTGACATCGATGGAAA
3596	TGCTGCTATTGTGCGACCGATATG
3597	TACAAAGAATCGGGACCTGCGACT
3598	GCGCCTCATCCCGCATCGAATTAT
3599	CGAGGGATTTTGACCAAGTGGATGA
3600	TGATAGGCATACGCGGAGAAGTCC
3601	CGAGTTGTCAACGGCCATCGAATT
3602	CCCGCACCGGATTATTAACGAACC
3603	TCGTCCTTGGGTCCCATGTAGAAA
3604	TCACGAAGCATCTTTGCGACGTAA
3605	TGTAAGTTGCCAACTTTGCGGGTT
3606	GCACACCACCGGCAGATATCAAGA
3607	GTGTGGTTTGTGAATGCGTGGTGA
3608	CAGCTGCGGGCCCCACCTTCGATAC
3609	CAGCGAAGGACGACTACTGTGCAC
3610	CAGCAGTTCGTTGCTTCCTGATTG
3611	AAACAATGGAGTGACCTCCCGCA
3612	ACTATACGAGCATCATGAGCCGGC
3613	CTTGATAAGGTGGGATTCCGGGCA
3614	TTAGTAGAACGCTGCGCGCGGTG
3615	AACTGACGTTGAATAAAACCGGCG
3616	GCTTTGTTCTACCGCGGATCATCA
3617	TGATATGCAGCGGCTCGGCCTTAT
3618	CGGGAGTGCGTTTATGTCCATGAT
3619	CAAATACCGGGAACGGATCGAAGC
3620	GATCAAGCCGAATGCTTTGCAAAG
3621	AGAGAGGATGCGCTCCGGTTAGAG
3622	CTTAGTCAGCATACCCGCGGGCAG
3623	GTGTCTCGGGGCGCAGGACCTGTA
3624	AACGCTCCACTGCCGTGATTCACT

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3625	GATCGTTGAGTCATCCCGTGGAGT
3626	CCTGGCCGGGTGCAATACTACAGT
3627	CGTAGCCCGAACGTAAGGGTCAGC
3628	CTGTGGCTTCAAGAGGATCCGTTG
3629	CTTGGGTCGGTGTAATGTCCTCGA
3630	GCCGTTGTGCGCTATTCTTACGGA
3631	TCGCACGATGGCTAGAACGAGTAA
3632	ATTTGTTGCAATGGGATGGCTCTG
3633	CGAATATCCGCTCGAACCTGACAA
3634	AAGTGGCGTGCGTCATAGCGCGAC
3635	TGATGTCCCTCCACACCGTGAAC
3636	CAAATGAAGTCGGGGCCAATATTG
3637	GATGCATAGCGTGATTCCGGTGTA
3638	GTGACCGTAGAAGCTCACCAGGGC
3639	ATAAGGACATATTCGGCCTGGGGA
3640	AGATCTCACAACCGGAACCGGACG
3641	GTTGCGTTTGGGGGCGTCATACAA
3642	TGTGAGGTTTTCCTAAGGCGAACG
3643	CATCTTGGTTTGCGAACGAACCTCA
3644	TTCCTGTCACAGATTCGTGGCCTT
3645	AACTTACCGATCCCTGAACGTGCA
3646	CCTATTCTGGACATGCGGCCACAT
3647	GTCGATGGGGAGCTCCAGTTGCAT
3648	CGACCGTGAGGGTCCATACGTAGA
3649	TCTCGTTTGACGCAACTGGGCCA
3650	ACTCCGCCGAATGAAGGAATAGCT
3651	CCTCGACCTGGCGTGATGGAAGGC
3652	TAACAGCCGTTTTCGCGTTCACAA
3653	GCCTCCTGCAGTACGGTGTCTGTT
3654	GGCAGTCGGTCCCACTTAGTTCTGA
3655	TAATCCACGGCTTTGGTGGAAGTC
3656	CGGTGCAAGATCCTGGTTGTGTGA
3657	TTTCACCACTACCTTAGGTTCGGCG
3658	CATCCCGTACCGGGAGGACAAGTC
3659	ACGAGGTAAAGGGATCCGTGCTGG
3660	CTAATAGTTTGGCAGAGGGGCGCT
3661	AGCATGGTAACCCTGAGCCAGCAG
3662	GGAATCCTTGTGGGAACAGCCGAT
3663	CTGATGTGGGAAAGAGGGTGGGAC
3664	ACTTTTTGCAATCCCGGCGTTGTA
3665	GCGATGACGTGACGAGTTCTCACC
3666	CCAGGTATTGAGCCCCGCCATATA

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3667	TTGGACGTCCTCCGAATATTGGCA
3668	GGTAAGTGCGGGAAGTACGCTGAC
3669	CCGCCTGAACCGTCGTAGGGATTA
3670	CGTTTTTGAGTAAGGATTGGGCGA
3671	TGTGGTATTGAGGCATAGGTGGCA
3672	TCCGGAAGGAAGGCGCGATATGGC
3673	GTTGAGCGAATCGGACGGCTTTAC
3674	TGAGTCTCCGAACGACAAGCGATC
3675	AGTGAAGAGGGAGAGTCCAACCCG
3676	GTGAAGCCTGACGAATCCAACGTG
3677	GTGCAGGCCTGTATCCCCATGACT
3678	GTGGGTTTCCTACACACCGGATGA
3679	GCGCCGTCGACTCTCTTCAGCTGC
3680	CTAGGCCTGCCATCACTGAGCAAT
3681	TTGGTGATGACTCATGGCCAGACC
3682	TATCTCCCGCGGGGTATATTACCG
3683	CCGAGGGACACGTATCCCTGTTCG
3684	TATCCCGCAGCACGCATTTCGATCT
3685	TGATGATAGAGCAGGGTGCCGTCA
3686	GTAGGAGCACACATTCGGATTCGG
3687	CCCTTACTACGCCCAGCCCTTTTG
3688	GTACCAGGGGGTGTGCTCCAAGGG
3689	TGACCAGGCGGACCAGACGGTTTT
3690	CGTAAGCGGCGGTAGGTGTGCTAC
3691	CGCGGGGAGGGATCAGCAGTTTTG
3692	AAAGCGTATCCAGAAAGGCCATGG
3693	AAGAAGAGACGCATGCTTGGACGT
3694	TGGCCATTTGCGGGAGGTGGCTTA
3695	AACGCCGAATTGAGGAGGCGGTTA
3696	GCCTCATTACGACATTGGCAGCAT
3697	TCGAACGCGATTTTGAAATGCCC
3698	AGGAATTCTAGCCGAAAGCCCTGC
3699	TCCGCTGGTTGGGTGCTCTGGTTG
3700	GTCGCGCTCCGTCCGATAGTATGA
3701	TGTGCAAGGACGGATGATTGCACT
3702	GGACAAGCGGCAACCTGGGAGAAG
3703	ATGCGGTGGCTACGGACTAATCCA
3704	TGCACGCAGGTGGAAAGCAGGCTT
3705	AGATTGTGGGAGTTGTCACGCTCC
3706	AACAGCAGTGAGGGCTGAAGCTTG
3707	CTGCCTGTTTCCTTCACGCTCCAT
3708	CCAATCCACTTGAGTCAACTTGCG



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3709	CATTCTACCGCCCAACTTTTGCAA
3710	CGGAGAACCATGCTGAGCAGTCCA
3711	GACTGTTCTCCAGAAAGGCGCAT
3712	AAATAATTGCTCCACGCGAAGCGC
3713	GGGCCTGGAAGACCAACCAAATAC
3714	ACGACGCGAGCACGTAGATATCAA
3715	TACGGGATCCTCGTGGCTACATCT
3716	CAAAGTCTCCCCGACCGAGTTGAC
3717	CCCAGGGCGAAGATCTCTAGGCAC
3718	CAAATTCTCGCCACGAGACCCTA
3719	CTGTGCGCATTCCAAACACATCAC
3720	CATGGAAATGCCAGCTGCCTCCAT
3721	CGCGAAACCACAGTCCTCGTCGGG
3722	GTCCGCAGCTGTCCCGACATTGGT
3723	GTCTCATTGGGACGATCGTCTCGA
3724	AGAGCGTTGCATGCTTGGCTGCGG
3725	CTCCGCCCTGTTCGCAATGAGG
3726	TTGCGGTTCATACCGAAGCCAACA
3727	TGCGCGAGAATCGTTCGTACGACG
3728	TGTATACCGTAGGCGTCCGTGGGG
3729	TGCGGGGTATAGGGCTTCCTTATG
3730	ATCCAGCCCAAGCAGCAGACGCA
3731	GTTCTTGGCCACAGGAATGGCCGT
3732	CACATGGGCATTAATTGCTACGGC
3733	ATAAGTCGGTCTGCCTGGCAATGA
3734	ACCTCGAGGCTGAGAACGTCAAAA
3735	GCGGAACGCTAGCCCCTTATGGTT
3736	TGCGAGGCTCCTGGAGCAATCCAA
3737	ACAGAAGGGCGATCGCTCTGGCTG
3738	GGTTGGCAAGGGGCCAGCTCCTAC
3739	ATCGCTTCGCTCTATGGAGTCCGA
3740	CGTCCCGATAGGCCGCCTTGATCT
3741	GAATTCTGAGGCGGCATTGTCCAC
3742	CAGCCCATCAGTATCGGCTGCGTA
3743	TGGAGAGTCGGATCCGTAGCGTCA
3744	TGGATCCAGTGCGAGTCTTGCCCG
3745	ATGCGGTCGTGCTTGAATCCTCT
3746	ATCGCACTGCCGCGTCATAACAGC
3747	CACGTCTCCGCCGGAACACAACCTG
3748	AAGACAGTGGGTGAACGCACGGTA
3749	ACGCGCATAGGTGGTCAAACATCG
3750	CCCGGCGGTAGAAATTGACAACCT

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3751	AAGGGATACTCAGGCGCCTGTTTT
3752	CTTCTCTCTTGTGCGGGCTCCCGT
3753	TTGAAGGGACCTGCCAAATGGCGA
3754	ACGCATGACGACGTCCAGTACGGG
3755	AAATGGATGTTACGCCGGCAAGCT
3756	TCGTGCGAGGCCTCTTCGGCATAC
3757	TACATCGCGTCGAGTCATTCTTGG
3758	TCACACCACATAATGGCACCACGT
3759	CAGGTTACGGTTGAGGAGTGCGA
3760	GGTGTTACACCGCTTCGTTGTCCT
3761	ACAATAATAAGGGAGCATCGGCCG
3762	TCGGGTCTATGATCCAGTCCCAA
3763	ACCCATTCTCTCGCGCGATCAA
3764	TCGCAGGTGTAGACGACGAAAAG
3765	CTCTTGCGTAGTAATCGGCCCGCA
3766	TTCCGTGTCACGCGAGCCTGCTTT
3767	ACTCTAAGTAGGGCTGGGTCGCGA
3768	TTGGTGGCTGTAAAGGTGCTTGGC
3769	CCGAATTACCCATTCATACGGCAC
3770	GATGGATAGGTTCGCTTCCCGCAA
3771	ATGACGGAAAGAATGTGATTCGGC
3772	ACGGTTCGGCTTCTGTTAGTCACG
3773	GGATCCCGTAATTGAGGCGGCCAC
3774	ACCCGTTAAGTCGACGCCTGCGGG
3775	TTCGATGTGAACGGTTGGCCAACC
3776	TCGATCGGGAGTCTACCGCCATGT
3777	AGCAACGAGTTTATGAGCGCAGGA
3778	TGGGAAACGAATGGGTGGCGGTTG
3779	TCTGTGTTGCCCCACCTACAGCAA
3780	CCTGCATTGGATGTACCCGCGGGT
3781	GAACGAGGTCCGGGTTTGCATCTC
3782	GGCGCCGAAGCAGAACGACCATAT
3783	AGGCATCACGCATCAGGTAATTGG
3784	TTTACAAAAGCATCGGCCCTGGGA
3785	CCCAGGCGGTCAACCAATTGTAGA
3786	CTGCAGCACGTGCCTGAAATTCGT
3787	CCGTTTTGCTCCAGCTATGAGCGT
3788	ATTTGTGCCGCATTGGGGTTATTC
3789	TAAGCAGAAAGCCGCAACTCCGGT
3790	GCGACTGATATAGTGCTCGGACCG
3791	AACTCTATTCTGACACCGCCCGAA
3792	GTGCGCTCCAAGAAGAAACACACC

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3793	ACGACCAGCGGTCTGAGATCTAGG
3794	ATCCCCTCCTCAGGTCGACGCTGT
3795	TGACATACGCGTCACCCAGCACAG
3796	TAACCGCGACTCTGACTCCCTTGT
3797	AAGCGGTTTGATCTGTGCAATCGG
3798	CTGTCAACTCGGTCGTCCGCACAG
3799	AACTTTGCCGTTTAGGGCAGGTGA
3800	GCTGAAGAACTCCCAATTCGCTGG
3801	AAGATGCGATGGGTCAGTCCTCGT
3802	ACCCACCTCTGAAGGTTGAGACGG
3803	AGGCTACGCACCCTCGAGAGTGAC
3804	CGGTCACGAACGTGGTCCAGTTTT
3805	CAAAGCAACGCGCGCCACTTAAAA
3806	ACGAGGAAGGAACTGATCCCCAGT
3807	TTCGCCACTATGGGCTCAGCATT
3808	CGCTCGGCAGAGGAGTCCACTCAC
3809	TGTTGGCACGACTCCGTCCATGAA
3810	TGCCTACCCGGTGATTGCGACATC
3811	CAACGGTCGGATCTGAGGAGATCT
3812	CGTTACGAAGCGAAGTTCCCGAGT
3813	AGTGACGGCCAAAGTCGCCATTCT
3814	ATTCAGCTGGGCATAGGCGATGGG
3815	TAGGACAGCGTGGCTGGCTACACA
3816	AATTTGTCCAGCTCTGCACGACCG
3817	TGAGTGGGCTGTGATCCGTTCCAC
3818	TGTGGTGACACGCCAGAGCTGGTT
3819	CCTCACAGGTGTGAGAGGAGCCGC
3820	AGTCCCGCTTCTGCAAATTCGGAA
3821	TCTGCGCCTACCCGTAAGCTGAAC
3822	GCCTCCTGAGTTGATTCATGCATG
3823	CCTAACGGTTGGTTCGCCGTTTTT
3824	TCGCAAACCCACGAATGAGTCCCG
3825	AGTGCTAAGGTGGGCGAGCAGAGG
3826	CTGGAGACTGCGATGGCAGGGTTG
3827	AAGGGATAGTGATGGCGATGGACG
3828	CTATCCACGGTGATGTCCGCCATT
3829	CGGACTAGAACTTGCCAAGCACGA
3830	AGAGCCGGATGGCATTGCATGAAC
3831	AGTTGGCTAGCGGTGGAATGAGCA
3832	GCATGCGGTACCGCTTCATCTAA
3833	GTGAGATTCCAAGCTCGCCGGTGA
3834	GCCATCCACCGCACAAATGAACGCT

3835	GGGTGGTCCTCACTGTGGTTGGCA
3836	AGGCGGCTACGACGAGCGTCGTTA
3837	GCCAAGTGATCGTGCTTCCGCGTA
3838	TAGCCGTTTATTCCCTTGATGCGC
3839	ACTATGTGGGACGAGCGTCTGCGA
3840	GCACCTTCGAGAACCCATCAGATG
3841	ATTTTCTGTACCGATGCTCACCGG
3842	CACTGGAGCAATAAATGGCCAGGC
3843	GGGTTACGTATCTCATGGATGCG
3844	GCACGCTCCAGTATGCTCCTTCA
3845	GAAGGGACTTAGTCCGCGGCCCTC
3846	TTCGTTACCCTAAGGGCGTTTGCA
3847	GTTCCAGGTCACGACGAGCTGCGC
3848	TCGTACGTAGTCACACGCGACTT
3849	GGGCTGGAGTAGCGGTCTGCTATG
3850	TAGCGGCACTCGTGTTGCGAGTGG
3851	ACGTTGGGTTCTGACACGGCGATT
3852	TGTTGCTGCGCCCCAAGTGATCTT
3853	CCCAGGTCGTTACGGTGCATCACA
3854	CCTAGTGCACAGGCAAATCGGGCT
3855	GGCGTTCTCCAAGATAAGGCCAAA
3856	ACTTCGATACCGTGGACCTCGCCA
3857	CTGAGCGCGCTAAACGTCCCTAGC
3858	ATCAGATAAACGATCCGACGCGTC
3859	CATGGCTGAATTTGTCGACCCTCT
3860	CGAAAGCGAGCAAATAGAATCCCC
3861	AGATTGCCCTGCGGCAGGTTGAAT
3862	AAGAGCGGCGCGATCAGTTAGAAA
3863	CTGATGCCTGTAAGGAGGCGCTCG
3864	AATCGCGAGGTTGCGCAGACAAAG
3865	CGTTGGGACACGGACCGTTCACTC
3866	AGATGTGTGCACTCGCGGTCATTT
3867	CAACTCGAGTGGCGGTAACATCTG
3868	ACCAAGGTTGCGATTACGGGAAGC
3869	CGAAGCGGTAGACGGCTCGCGTTA
3870	TCTCGCGAACAGGAGGGAAGGCGT
3871	GTCCCGATTTGCGCTGTGAGGAAA
3872	TACCACGCGTCGGCACGGAAATGG
3873	AAATGCTACCCGATTGCGCGGGAT
3874	TCGATTCAGGTTTGTGCTGCGGAG
3875	CCATCTCATCCCACTATGGCATGC
3876	CTGGCCCGTGTTTGTTGAGTCGA

3877	GACACACACGTTGCAGGGCTTCCC
3878	TCGAATCGAGTCGATCGTGAAGGT
3879	GAAAGCACTCGATCGCGTTGGATT
3880	AATTACGCGAACATGGGGCGTCAA
3881	GTGCTAACACTGTGGTCGTTCCCA
3882	GGTAAGCGCCAGCCAGGAGTTGTC
3883	GGCGATCGTTCAGGAATCGCGTCA
3884	CTGGCTAGACCTCCGACACAGGCT
3885	CGGGTTAAACGCCAACTGGCCTAG
3886	ATCGCAGCCTGGCCGCCTAGTTTT
3887	GGCGTAGCCTAGCAAATTATGCCA
3888	ATGACGCGACGGAGACAATACGGC
3889	GTTGCATCACGAAAATGCCGTCTT
3890	GAGTCATGCGTTCCTCGCTTTACC
3891	TCTGAACCGGTTATCCCCAACCTC
3892	TGCCTCTGGTAGGCGCCAGTTAC
3893	CTGACGGTTTTATTGCGCGTGCC
3894	TGAACACGAGCAACACTCCAACGC
3895	CGGCGCGCGAAAGACTTGAAC TTG
3896	GCTACGAGTACCCGTCGGAACGC
3897	ATACCCAACAGCATGGAGCGACCA
3898	ATCGCATCGCATCGTATTCACGGG
3899	CGGCCTAGAGGTGCGAAAGCTATC
3900	TAACGCTTTTCCGAGGCCGATTCT
3901	TCTGTCCTAGCACGCCGACCTGCT
3902	CTCATCGTTCAGTCGGTCGTCGTA
3903	TCGTCGAGCAGATAGCGGGGTAGG
3904	TCGACCACAGTCAGGACACTACCG
3905	TGCGATTCTATGATGTCCGAACGC
3906	CAAATGCAATGGCAAGCACTCACC
3907	TCTAATCCATCGTTTTTGGGCGA
3908	TCTCAACTCCGGTACGACGAAACA
3909	CTGAAGAGGGTAGCCTGGGAGCGG
3910	GGCACAATTAAACGCGCCGCGTT
3911	CAAAGGAGGGTCAAAGGCCAGAAA
3912	TTTGCGGCCGTGACGAGCAAAAAT
3913	AGGAATGTGCGTGGCACCTGTGGA
3914	TCGTGATGACTGCCTTCCGAATCA
3915	CACGTCGACATGTTTGGTACCTCG
3916	TTGCGGTAGTTTGGTTACCACCGT
3917	GCA GTGGCGACAAATACAGCTGAG
3918	ACGGCATGATGGAGGGATAAACGT

3919	TGGGATAATCCGCAAGCGCATAGC
3920	CCTAGCTCTGCTGCGTCTTTGCGC
3921	TCCTGGAAGTCTGAAGGCGACTT
3922	CGAAGGCGGCATGGTGTAGTCTCC
3923	AACATTGTTCCCATCCCAGAGCAC
3924	CCAGGCAAGAAACAACCACGCGCT
3925	AAATCCACAGGCGCGCCAAAGCTG
3926	GCTCACCGCAGACTCCGCGCGATA
3927	TAGGTGGCGAGAGAGCGCCACAA
3928	GGCGTTGGTGTGTCGGGACCATGA
3929	TCTGAATGCTTCCGTGCTTTCGTG
3930	ACGCTCTGGACCTCGCTCATTCTGA
3931	TCCTTTATGCGCAGCGCTCGTGTT
3932	TTGCCGTCCTGCAGCAGGTAGCTC
3933	GGTCTAGTGGCAGCAAGGAGCGAT
3934	GGTAACGCGACCAGCTTAGACACC
3935	GTGGCGATTGGCTTCCTATGCATA
3936	TCAAATACGGCCAGGAAGGGCAA
3937	TGCCATGCAGTCAGGTACGATGGT
3938	ACAGGTTACGTCGTGTGTTCCCGT
3939	CTCATGACGAACGAGCGGTCTGCA
3940	GTCGTGCGAGAGGCCAAGACCTTA
3941	GCTGGCTGACGCTGTTGTCAGAGG
3942	GCTACAGTGCTGCGTCCCGTGCCT
3943	TTTACGAGCACCAGCTGGCGTAG
3944	ACGAGTTGACGGTCGTAGGGACCG
3945	TCGGATGGTAGGAGGCGAGATCGG
3946	ATTATGCAGATCCTGTGCATCCGC
3947	AGGGATGGAGACGAAGGAAGCATT
3948	ACCCAGGACCCGTATTCCCTAGC
3949	GCACCATCCTGGGGCTTCTCAATG
3950	TACAATCCGTGGACGTTTGCTCAG
3951	GGTAGGCGAATCCGACTGGCATAG
3952	AGGACCGAACCCATGTGCAGCATC
3953	ATACACCGCACAGAAGCACAGCTG
3954	TCCTTGCGGCGCGTGTGTTTATTG
3955	CTCCACGCGAAGGGCGCTTGTAAC
3956	TGGCCCTGCCATCCTCGGATTCTAG
3957	TGTCTATTGCCAGCGTGAGCATC
3958	TGTTGTTGGCACGCCTCTACGGCA
3959	GTGCCTCAACCGTATCGTGGCGGT
3960	TCCTCGAAGTAGCGTGACCGAACC

3961	AAACAATTCCTGCACTCTCGGCC
3962	CACAACTCGTCGAGGCACACAGT
3963	GACGAAACGCTCGGCAGAAAGCCT
3964	TCAACTCACACGGGACAGCAGTTC
3965	TCACGTGGATGGGCTTAGCTGGGC
3966	AGGTGTTTGTTCGACTGGCCACA
3967	TCAACCCTCTATTCCCAGCATTG
3968	ACCTCACACAAGCGTTCTCGTCGA
3969	AACAGCATGCGGTCGCTGGCTTTC
3970	CACGGACACGTGTTACATCCGATG
3971	CTGGGAGCCTGCTGATACATGGTG
3972	CGTCCTATGGGCCATGGCCAGGAT
3973	GTCCCCAAATCTCGCTTTACAGGC
3974	TCACAAACCTGTGCGTGCAATTGTC
3975	CACACTCGTGGCCTGCGTTGGGAA
3976	GCCTGCACTTACGGCTATCTCGCC
3977	TTGGCGTGGCGATTACCTGTTATT
3978	TTTGCGGCTGAAGTTTACAGGGTG
3979	CACCTAAGGGGCTGACCGAGCAAC
3980	AGAAAACGTCAATCCGCCACCTTT
3981	AACAAAACGGCGCTCCAACAAACG
3982	GCCTCAATATCTGGTTGCCGCCTG
3983	TTCCACAGTCAATGATGGGCGTGC
3984	GATTCCCAGTCTACCCGCGAGCAT
3985	AGGCCAATTACGACCCTGTCACGG
3986	CATGCGAACGTTCCGAGGAGACGG
3987	CACACGCGATGGGTTGTGTGACGC
3988	TCCGGTATTGCGCAGGAACCATAG
3989	AAGATTAGGTGTGCCCGCCTCAGG
3990	TCGTTACGCCCCGACTCGACGATG
3991	ACTAAAATCGCCAGGTTGCTCCCT
3992	AGGATGGCCACGCCGAATCAAAGT
3993	TGATGAAGCAGCTCATCGCTGGCG
3994	CCCCGATGGGTCTTTGTTGGAATC
3995	ACACGAGGGCTGCTGGTGAGGGCT
3996	TGGTCACCAATTTGATGATCCGAG
3997	AAGGCCGCTTGCATGCGACAAATT
3998	CCAGTGTTGTTTCATCGGTGGCGT
3999	CCGACCGCTACATAGGTGTGCGAA
4000	TGTTGAAGCCGTTCCAGATGACA

TABLE 2

Seq. ID No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
1	TTCGCCGTCGTGTAGGCTTTTCAA	TTGAAAAGCCTACACGACGGCGAA
2	TTCGAAGCGCACGTCCCTTTTCAA	TTGAAAAGGGACGTGCGCTTCGAA
3	AACGCGTGGGGAATGGGACATCAA	TTGATGTCCCATTCCCCACGCGTT
4	CCGTCGCATACCGGCTACGATCAA	TTGATCGTAGCCGGTATGCGACGG
5	ATGGCCGTGCTGGGGACAAGTCAA	TTGACTTGTCCCCAGCACGGCCAT
6	TTGCAACGGGCTGGTCAACGTCAA	TTGACGTTGACCAGCCCGTTGCAA
7	CGCATAGGTTGCCGATTTTCGTCAA	TTGACGAAATCGGCAACCTATGCG
8	CCGTTTGCGGTGCTCCTTGCTCAA	TTGAGCAAGGACGACCGCAAACGG
9	TTCGCTTTTCGTGGCTGCACTTCAA	TTGAAGTGCAGCCACGAAAGCGAA
10	GTCCAACGCGCAACTCCGATTCAA	TTGAATCGGAGTTGCGCGTTGGAC
11	TTGCCGCACCGTCCGTCACTCAA	TTGAGATGACGGACGGTGCGGCAA
12	CATCGTCCCTTCGATGGGATCAA	TTGATCCCATCGAAAGGGACGATG
13	GCACGGGAGCTGACGACGTGTCAA	TTGACACGTCGTGAGCTCCCGTGC
14	AGACGCACCGCAACAGGCTGTCAA	TTGACAGCCTGTTGCGGTGCGTCT
15	CGTGTAGGGGTCCCGTGCTGTCAA	TTGACAGCACGGGACCCCTACACG
16	CATCGCTGCAAGTACCGCACTCAA	TTGAGTGCGGTACTTGACGCGATG
17	GGCTGGTTTCGGCCCGAAAGCTTAG	CTAAGCTTTCGGGCCGAACCAGCC
18	GTTCCCACTGAAGCTGCGATCTGG	CCAGATCGCAGCTTCACTGGGAAC
19	TACTTGGCATGGAATCCCTTACGC	GCGTAAGGGATTCCATGCCAAGTA
20	ACTAGCATATTCAGGGCACCGGC	GCCGGTGCCCTGAAATATGCTAGT
21	GAACGGTCAATGAACCCGCTGTGA	TCACAGCGGGTTCATTGACCGTTC
22	GCGGCCTTGGTTCAATATGAATCG	CGATTTCATATTGAACCAAGGCCGC
23	GATCGTTAGAGGGACCTTGCCCGA	TCGGGCAAGGTCCCTCTAACGATC
24	TGGACCTAGTCCGGCAGTGACGAA	TTCTGCTACTGCCGGAAGTCCA
25	ATAAACTACCCAGGACGGGCGGAA	TTCCGCCCCGTCTGGGTAGTTTAT
26	CATCGGTTTCGCGCCAATCCAGATA	TATCTGGATTGGCGCGAACCAGATG
27	GTCGGGCATAGAGCCGACCACCT	AGGGTGGTGGCTCTATGCCCGAC
28	CTTGGGTCATGATTACCGTGCTA	TAGCACGGTGAATCATGACCCAAG
29	TGCCTAACGTGCTAATCAGCAGCG	CGCTGCTGATTAGCACGTTAGGCA
30	CGCATGTTGGAGCATATGCCCTGA	TCAGGGCATATGCTCCAACATGCG
31	AGCCACTGCATCAGTGCTGTTCAA	TTGAACAGCACTGATGCAGTGGCT
32	GGTTGTTTTGAGGCGTCCCACACT	AGTGTGGGACGCCTCAAAACAACC
33	TCGACCAAGAGCAAGGGCGGACCA	TGGTCCGCCCTTGCTCTTGGTCTGA
34	GACATCGCTATTGCGCATGGATCA	TGATCCATGCGCAATAGCGATGTC
35	GAAATACGAAGTCTGCGGGAGTCG	CGACTCCCGCAGACTTCGTATTTT
36	TGTCATGAATGATTGATCGCGCGA	TCGCGCGATCAATCATTATGACA
37	ATATCGGGATTGTTCCCGGTGAA	TTACCCGGGAACGAATCCCGATAT



38	GCGAGCGTACCGAAGGGCCTAGAA	TTCTAGGCCCTTCGGTACGCTCGC
39	TTACCGGCAGCGGACTTCCGAATT	AATTCGGAAGTCCGCTGCCGGTAA
40	GTAATCGAGAGCTGCGCGCCGTCT	AGACGGCGCGCAGCTCTCGATTAC
41	CCTGTTAGCGTAGGCGAGTCGATC	GATCGACTCGCCTACGCTAACAGG
42	TAGCGGACCGGCAGAATGAGTTCC	GGAATCATTCTGCCGGTCCGCTA
43	GGTACATGCACTACGCGCACTCGG	CCGAGTGCGCGTAGTGCATGTACC
44	AATTCATCTCGGACTCCCGCGGTA	TACCGCGGGAGTCCGAGATGAATT
45	GCCAAATCTGGATTGGCAGGAATG	CATTCTGCCAATCCAGATTGGC
46	TGCATTTTCGGTTGAGGCACATCC	GGATGTGCCTCAACCGAAAATGCA
47	CCGCTCAATTCACCATGCTTCGCT	AGCGAAGCATGGTGAATTGAGCGG
48	CTCGGAAAGGTGCAACTTTGGTGT	ACACCAAAGTTGCACCTTTCCGAG
49	AATTCGACCAGCAGAACGTCCCAT	ATGGGACGTTCTGCTGGTCAATT
50	GCCAGAGTCTCAACCTCACGGGAT	ATCCCGTGAGGTTGAGACTCTGGC
51	CCAACAACCTGGAACGGGAACCGGC	GCGGGTTCCCGTTCAGTTGTTGG
52	GAGAACTGATCGCTGAGGGGCATG	CATGCCCCTCAGCGATCAGTTCTC
53	GGCACACTAGACTTGTGGCACCGA	TCGGTGCCACAAGTCTAGTGTGCC
54	TCACATCCAAATATGGTCCGCGAA	TTGCGGACCATATTTGGATGTGA
55	GTCTGCCGGTGTGACCGCTTCATT	AATGAAGCGGTACACCGGCAGAC
56	CATCGCAGAGCATAAACACCCTCA	TGAGGGTGTATGCTCTGCGATG
57	GTTGGTATCTATGGCAGAGGCGGA	TCCGCCTCTGCCATAGATACCAAC
58	ACGAGGTGCCGCTGAGGTTCCATT	AATGGAACCTCAGCGGCACCTCGT
59	GGAATGAGTGGACCCAGGCACATT	AATGTGCCTGGGTCCACTCATTCC
60	TGTCAATATGCGTCCGTGTCTCT	AGACGACACGGACGCATATTGACA
61	TGATGAGCCTCAGGGTACGAGGCA	TGCCTCGTACCCTGAGGCTCATCA
62	CACCGCGGTGTTCTACAGAATGA	TCATTCTGTAGGAACACCGCGGTG
63	TTGTTGCCAATGGTGTCCGCTCGG	CCGAGCGGACACCATTGGCAACAA
64	TTAACCTGCGTCTGCCCTTTCT	AGGAAAGGGGCAGACGCAGGTAA
65	AGGCGCGTTCCTGCCTTAGTGACG	CGTCACTAAGGCAGGAACGCGCCT
66	TAGGGCGATGGCACGAAGCTTCAA	TTGAAGCTTCGTGCCATCGCCCTA
67	TGCATAGAGCCAAAGTCGGCGATG	CATCGCCGACTTTGGCTCTATGCA
68	TTGAGAGGCAGGTGGCCACACGGA	TCCGTGTGGCCACCTGCCTCTCAA
69	TCCGCATTGTGAGAAAAACGAGC	GCTCGTTTTTCTCACAATGCGGA
70	GGCGGTTTCCGTAGCTATAGGTGC	GCACCTATAGCTACGGAAACCGCC
71	GGTGAAAATTTCTAGCCACGGGC	GCCCGTGGCTACGAAATTTTACC
72	CCGACGGAGGATGAAGACAATCAC	GTGATTGTCTTCATCCTCCGTCCG
73	CCAGTTTGCCCAATTCGCCAAAA	TTTTGGCGAATTGGGCCAAACTGG
74	GGATCTATTAGGCCGTGCGCACAG	CTGTGCGCACGGCCTAATAGATCC
75	CGGATGTCACCGTTTGGACTTTCA	TGAAAGTCCAAACGGTGACATCCG
76	ATCGCAAATCCTGCTCGTCCCTAA	TTAGGGACGAGCAGGATTTCGGAT
77	CAGGGCATGCAATAATCGAGGTTT	GAACCTCGATTATTGCATGCCCTG
78	CATGCGTTGATATATGGGCCCAAG	CTTGGGCCCATATATCAACGCATG

79	CAGCTGCAGCTTGTGACCAACCAC	GTGGTTGGTCACAAGCTGCAGCTG
80	TTGTATGTCTGCCGACCGGCGACC	GGTCGCCGGTCGGCAGACATACAA
81	GATGGCGCCCGTTGATAGGTATGG	CCATACCTATCAACGGGCGCCATC
82	ATGAGAATCGCCGGCAATCTGCTA	TAGCAGATTGCCGGCGATTCTCAT
83	ATTTGCACTGACCGCAGGCTCGTG	CACGAGCCTGCGGTCAGTGCAAAT
84	CAGGGAGAACGGTTAAGTTCCCGT	ACGGGAACCTAACCGTTCTCCCTG
85	AGGCCGGCGATCGAGGAGTTTGGT	ACCAAACCTCCTCGATCGCCGGCCT
86	ACACGGTGGTCTCTGATAGCGACC	GGTCGCTATCAGAGACCACCGTGT
87	GTGCAACGCCGAGGACTTCCATCA	TGATGGAAGTCTCGGCGTTGCAC
88	TCGGTGCCTGATAGCCATTCCGAT	ATCGGAATGGCTATCAGGCACCGA
89	TGAAATACCACACAGCCAATTGGC	GCCAATTGGCTGTGTGGTATTTC
90	GCATCGTGTACATGACTGCCGCGA	TCGCGGCAGTCATGTACACGATGC
91	CAGTGTCTAACGGCGCGCGTGAA	TTACGCGCGCCGTTAGAACACTG
92	CGCTTGCAACGTTGCACCTACTCT	AGAGTAGGTGCAACGTTGCAAGCG
93	CGAAAACTAGTGGGCTCGCCGCG	CGCGGCGAGCCCACTAGTTTTTCG
94	CTTTCAGGGGAACGCGGAGTCG	CGACTCCGGCAGTTCCTGAAAG
95	TTGTGGCCTTCTTGTAAGGCACG	CGTGCCTTTACAAGAAGGCCACAA
96	TCCACGAACGGCGACCCGTTGTCT	AGACAACGGGTCGCCGTTCTGGA
97	CGACCTTGACAGAAACCTAACGAG	CTCGTTAGGTTTCGTGCAAGGTCG
98	GTGCAGCTTCACGAGCCAGCCTGA	TCAGGCTGGCTCGTGAAGCTGCAC
99	CGCTTTCGTGCGAATAGACGATGA	TCATCGTCTATTTCGCACGAAAGCG
100	TGCGCTTACAGGCTCCTAGTGGTC	GACCACTAGGAGCCTGTAAGCGCA
101	CACGCGCTTAGTCGCGATCGCATA	TATGCGATCGCGACTAAGCGCGTG
102	CGGAGGGAGGGAGCTAGCCTTCGA	TCGAAGGCTAGCTCCCTCCCTCCG
103	GCATCCGGCCTGTTGATGACGCCT	AGGCGTCATCAACAGGCCGGATGC
104	AGGCCAATCGATCTTATTGCCGAG	CTCGGCAATAAGATCGATTGGCCT
105	CCTTCCAATGATTGCATACGCCCA	TGGGCGTATGCAATCATTGGAAGG
106	AACACTTGATCAGGCGGGTCTGTCT	AGACGACCCGCCTGATCAAGTGT
107	TGGAATCAAGGCCGTAAAGGACAG	CTGTCCTTTACGGCCTTGATTCCA
108	GCTCCCGTAACCTGTCCACCAGTG	CACTGGTGGACAGGTTACGGGAGC
109	AGTGGTGAATGGCCGTACCCTGA	TCAGGGTAGCGGCCATTACCACT
110	TGTTGAAGCGAGCTAAAACGGCCA	TGGCCGTTTTAGCTCGCTTCAACA
111	CAGCGCTCCAGAATTGACAGCAAT	ATTGCTGTCAATTCTGGAGCGCTG
112	AAGGTGGTGCCATTCAATTGGCTA	TAGCCAAATGAATGGCACCACCTT
113	CGTTAAACCGCAATCCGTTCCGCT	AGCCGAACGGATTGCGGTTTAACG
114	CACGAGATACGGGCGTAAGGGTGG	CCACCCTTACGCCGGTATCTCGTG
115	CTACGGCAAACGTGTGGAATGGGT	ACCCATTCCACACGTTTGCCGTAG
116	GTAGGGCGATGACGGGCGAACTAC	GTAGTTCGCCCGTCATCGCCCTAC
117	AATCGACCTCCGCACACATTCCGA	TGCGAATGTGTGCGGAGGTCGATT
118	GAGTCAGCATGGCGGCGGAGATTC	GAATCTCCGCCGCCATGCTGACTC
119	AGATAAAGACGCTGGCAACACGGG	CCCGTGTGGCAGCGTCTTATCT

	120	GGTACCTCAACGCGAACCACTTGT	ACAAGTGGTTCGCGTTGAGGTACC
	121	AAGCGATGGCTACCCAAGAGCGAT	ATCGCTCTTGGGTAGCCATCGCTT
	122	AGAGCTTATGCAGAACCAGGCGCC	GGCGCCTGGTTCTGCATAAGCTCT
5	123	ATCGGTCTCACGCAGGGTTGGATA	TATCCAACCCTGCGTGAGACCGAT
	124	TAGGTTGCCCGCCAGAAGAAACAT	ATGTTTCTTCTGGCGGGCAACCTA
	125	CGGTGCTGTTGCAAAAGCCTGTAG	CTACAGGCTTTTGCAACAGCACCG
	126	TGATGAAAGTTTGCGGCAGGACAC	GTGTCCTGCCGCAAACCTTTCATCA
	127	GTTGAGTGCAGGATGCAGCGATAG	CTATCGCTGCATCCTGCACTCAAC
10	128	AACATTGCGCGGTCCACCAGGGTT	AACCCTGGTGGACCGCGCAATGTT
	129	GGGCAGTTAGAGAGGGCCAGAAGT	ACTTCTGGCCCTCTCTAACTGCCC
	130	TCGAGCTGGTCCCCGTGAACGTGT	ACACGTTACGGGGGACCAGCTCGA
	131	GTCTTGGGGGCGCGTTAGTGAAAA	TTTCACTAAGCGGCCCCCAAGAC
	132	ACTGTTGGCTTGCTCTCATGTCCA	TGGACATGAGAGCAAGCCAACAGT
15	133	AGGACCATTGGAAGGCGAAGATA	TATCTTCGCCTTCCGAATGGTCCT
	134	CTTGGGAGGCATCCGCTATAAGGA	TCCTTATAGCGGATGCCTCCCAAG
	135	AATAAACGGAACGCACCGCTACAG	CTGTAGCGGTGCGTTCCGTTTATT
	136	TTGTACGTGCGGTCCCCATAAGCA	TGCTTATGGGGACCGCACGTACAA
	137	CGCACCAAACAGAGTTTCCCAGAC	GTCTGGGAAACTCAGTTTGGTGCG
20	138	ACCTGATCGTTCCCCTATTGGGAA	TTCCCAATAGGGGAACGATCAGGT
	139	GGAACAGAGGCGAGGGGACTGAGC	GCTCAGTCCCCTCGECTCTGTTCC
	140	CCCTGCCTTGCGGTGTCGGCTTAT	ATAAGCCGACACGCCAAGGCAGGG
	141	ACTCTGACACGCCAACTCCGGAAG	CTTCCGGAGTTGGCGTGTCAGAGT
	142	CTGACGGTTTTTCATTGCGCGTGCC	GGCAGCCGAATGAAAACCGTCAG
25	143	TGCGGTGGTTCATTGGAGCTGGCC	GGCCAGCTCCAATGAACCACCGCA
	144	GCATGGCCAACTAGTGACTCGCAA	TTGCGAGTCACTAGTTGGCCATGC
	145	AGGCCGTAAAGCGAATCTCACCTG	CAGGTGAGATTGCTTTACGGCCT
	146	CGAATATTATGCCGAGAATCCGCG	CGCGGATTCTCGGCATAATATTCG
	147	ACAGACGAGCTCCCAACCACATGA	TCATGTGGTTGGGAGCTCGTCTGT
30	148	GGACGGTTTTGTGCTGGATTGTCTG	CAGACAATCCAGCACAAACCGTCC
	149	AAAGGCTATTGAGTTGGTTGGGCG	CGCCCAACCAACTCAATAGCCTTT
	150	GATGGCCTATTCGGAGATCGGGCC	GGCCCGATCTCCGAATAGGCCATC
	151	GATCCAGTAGGCAGCTTCATCCA	TGGGATGAAGCTGCCTACTGGATC
	152	AATAACTCGCGCGGTATGCTTCT	AGAAGCATACCCGCGCGAGTTATT
35	153	GGAGGAGGTTTGTCTCGGAAAGCA	TGCTTTCCGAGACAAACCTCCTCC
	154	CTTTGGTATGGCACATGCTGCCCCG	CGGGCAGCATGTGCCATACCAAAG
	155	AGAAAGGCTCGAGCAACGGGAACT	AGTTCCCGTTGCTCGAGCCTTTCT
	156	AATCTACCGCACTGGTCCGCAAGT	ACTTGCGGACCAGTGCGGTAGATT
	157	CGTGGCGGCCACAGTTTTTGGAGG	CCTCCAAAACTGTGGCCGCCACG
40	158	TTGCAGTTCAATCCATACGCACGT	ACGTGCGTATGATTGAACTGCAA
	159	GGCCCAAAGCCCCAGACCATTTTA	TAAAATGGTCTGGGGCTTTGGGCC
	160	CGCCTGTCTTTGTCTCCGACAAT	ATTGTCCGGAGACAAAGACAGGCG

	161	TGAGGCAACAGGGGCCAAAACTA	TAGTTTTGGCCCCTGTTGCCTCA
	162	AGCGGAAGTAGTCCTCGGCTCGTC	GACGAGCCGAGGACTACTTCCGCT
	163	GGCCCCAAGGCTTAGAGATAGTGG	CCACTATCTCTAAGCCTTGGGGCC
5	164	GCACGTGAAGTTTAACCGCGATTG	GAATCGCGGTAAACTTCACGTGC
	165	AGCGGCAGAAACGTTCTTGACGG	CCGTCAAGGAACGTTTCTGCCGCT
	166	TCGTGAGCAGACGAGATTGCACG	CGTGCAATCTCGTCTGCTCGACGA
	167	TCTTTGCCGCGTAACTGACTGCTT	AAGCAGTCAGTTACGCGGCAAAGA
	168	TTTATGTGCCAAGGGGTTAACCGA	TCGGTTAACCCCTTGGCACATAAA
10	169	TGTTACTGTGGTTCACGGCAGTCC	GGACTGCCGTGAACCACAGTAACA
	170	CGCGCCTCGCTAGACCTTTTATTG	CAATAAAAGGTCTAGCGAGGCGCG
	171	ACAAATGCGTGAGAGCTCCCACT	AGTTGGGAGCTCTCACGCATTTGT
	172	CGCGCAGATTATAGACCCGAATGT	ACATTCGGGTCTATAATCTGCGCG
	173	CAAATAACGCCGCTGAATCGGCGT	ACGCCGATTCAGCGGCGTTATTTG
15	174	CCTTCGTGCATCGGTGATGATGTT	AACATCATCACCGATGCACGAAGG
	175	TGAACACGAGCAACACTCCAACGC	GCGTTGGAGTGTTGCTCGTGTTCA
	176	CAGCAGATCCTTCGTAGCGGTCGT	ACGACCGCTACGAAGGATCTGCTG
	177	GGAACCTGGTGAGTTGTGCCTCAT	ATGAGGCACAACTCACCAGGTTCC
	178	TCATAAGCGACAATCGCGGGCTTA	TAAGCCCGCGATTGTGCGTTATGA
20	179	CCCAACGTCACTGAAGCTCACAGT	ACTGTGAGCTTCAGTGACGTTGGG
	180	TGTCAGAGCCCGCGACTCAGACGG	CCGTCTGAGTCGCGGGCTCTGACA
	181	TACACGAAGCCTCTCCGTGGTCCA	TGGACCACGGAGAGGCTTCGTGTA
	182	CTCAGAAGTCCTCGGCGAACTGGG	CCCAGTTCGCCGAGGACTTCTGAG
	183	ATCCTTTTATCTACTCCGCGGCGA	TCGCCCGCGAGTAGATAAAAGGAT
25	184	AGGCGTGCAGCAACAGGATAAACC	GGTTTATCCTGTTGCTGCACGCCT
	185	ACTCTCGAGGGAGTCTCTGGCACA	TGTGCCAGAGACTCCCTCGAGAGT
	186	TTGCCAGGTCCATCGAGACCTGTT	AACAGGTCTCGATGGACCTGGCAA
	187	TCCACTATAACTGCGGGTCCGTGT	ACACGGACCCGCAGTTATAGTGGA
	188	GCCCAGTCGGCTCTAACAAGTTG	CGAACTTGTTAGAGCCGACTGGGC
30	189	CGGAACGGATAATCGGCGTCAGGT	ACCTGACGCCGATTATCCGTTCCG
	190	TAAAATAAGCGCCTGGCGGGAGGA	TCCTCCCGCCAGGCGCTTATTTTA
	191	GCGCACTCGTGAAACCTTTCTCGC	GCGAGAAAGGTTTCACGAGTGCGC
	192	AGTTTGCCAGGTACTGGCAAGTGC	GCACTTGCCAGTACCTGGCAAAC
	193	ACAACGAGGGATGTCCAGCGGCAT	ATGCCGCTGGACATCCCTCGTTGT
35	194	TTTCGACGACCCGCTAGGTACAGT	ACTGTACCTAGCGGGTCTGCGAA
	195	TAACCCGATTTTGCGACTCTGCC	GGCAGAGTCGAAAAATCGGGTTA
	196	CGTCGCATTGCAAGCGTAGGCTTG	CAAGCCTACGCTTGCAATGCGACG
	197	GAGCTGACGTCACCATCAGAGGAA	TTCTCTGATGGTGACGTCAGCTC
	198	GGAGGCTGGGGGTCGCGCTTAAGT	ACTTAAGCGCGACCCCCAGCCTCC
40	199	TTGTGGGAACCGCACTAGCTGGCT	AGCCAGCTAGTGCGGTTCCACAA
	200	CCCTCGCACTGTGTTACCCTCTT	AAGAGGGTGAACACAGTGCGAGGG
	201	TCATTGACTCGAATCCGCACAACG	CGTTGTGCGGATTCGAGTCAATGA

202	ACAGGGGTTGGCCTTCGTACGTAC	GTACGTACGAAGGCCAACCCCTGT
203	AGGCCGTGCAACATCACACAGGAT	ATCCTGTGTGATGTTGCACGGCCT
204	GGGCCGTGGTCACGTAATATTGGC	GCCAATATTACGTGACCACGGCCC
205	GCGCGGACATGAAACGACAAGGCC	GGCCTTGTGTTTTATGTCCGCGC
206	CTTATTGGGTGCCGGTGTCCGATT	AATCCGACACCGGCACCCAATAAG
207	GGGGCGGTTACCAAAAAATCCGAT	ATCGGATTTTTTGGTAACCGCCCC
208	GCTAAAGCGTGCTCCGTAAC TGCC	GGCAGTTACGGAGCAGCCTTAGC
209	ATCTCATGCATCTCGGTTCTGCT	ACGACGAACCGAGATGCATGAGAT
210	ACGAAAAAGTGTGCGGATCCCCT	AGGGGATCCGCACACTTTTTTCGT
211	CCAAGTACACCGCACGCATGTTTA	TAAACATGCGTGCGGTGTA CTGG
212	ATCGTGCGTGGAGTGTCCGATCTA	TAGATGCGACACTCCACGCACGAT
213	TCCAGATACCGCCCCGAAC TTTGA	TCAAAGTTCGGGGCGGTATCTGGA
214	TCTGCTGGCAGCACGTGAAGTGGC	GCCACTTCACGTGCTGCCAGCAGA
215	TTGAAATTGCTCTGCCGTCAGTCA	TGACTGACGGCAGAGCAATTTCAA
216	AGTCAGGCGAGATGTT CAGGCAGC	GCTGCCTGAACATCTCGCTGACT
217	ACAAGCCGACGTTAAGCCCGCCCA	TGGGCGGGCTTAACGTCCGGCTTGT
218	CCCTAATGAGGCCAGTAACCTGCA	TGCAGGTTACTGGCCTCATTAGGG
219	GTGAGACACACATCCCTCCAATG	CATTGGAGGGGATGTGTGTCTCAC
220	CGACGGATGCAGAGTTCAGTGGTC	GACCACTGAACCTCTGCATCCGTCG
221	CCCGCATGCCTGGCGGTATTACAA	TTGTAATACCGCCAGGCATGCGGG
222	TTAGCAAAGCGGCGCGCTTAGCAA	TTGCTAACGGCGCGCGCTTGCTAA
223	CCCGACACGGGT CAGCGTAATAAT	ATTATTACGCTGACCCGTGTGCGG
224	GCGACGGCCCTGAGGTATGTGCTC	GACGACATACCTCAGGGCCGTCGC
225	CAAAAGTGTGTTCCCTTGCGCTTG	CAAGCGCAAGGGAACACACTTTTG
226	TCTCGAAGCACAGCCCGGTTATTG	CAATAACCGGGCTGTGCTTCGAGA
227	ATGCTAACCGTTGGCCATGGA ACT	AGTTCCATGGCCAACGGTTAGCAT
228	CTTGCGGAGTGTTAGCC CAGCGGT	ACCGCTGGGCTAACACTCCGCAAG
229	TGCTCCCTAGGCGCTCGGAGGAGT	ACTCCTCCGAGCGCCTAGGGAGCA
230	CCAATGCCTTTGAGTAAGCGATGG	CCATCGCTTACTCAAAGGCATTGG
231	AGCAGATAACGTCCCAATGACGCC	GGCGTCATTGGGACGTTATCTGCT
232	TTGACCATTACGTGTTGCGCCCAT	ATGGGCGCAACACGTAATGGTCAA
233	TCGCGTATTTGCGGAATTCGTCTG	CAGACGAATTCGCAAAATACGCGA
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235	TCTGGTGCCACGCAAGTCCACAG	CTGTGGACCTTGCGTGGCACCAGA
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237	TTTTCGTGATTGCCCGGAGGAGGC	GCCTCCTCCGGGCAATCACGAAAA
238	TCGGGATGTAGCTGGGGCTACCGG	CCGGTAGCCCAGCTACATCCCGA
239	CGAGCCAACGCAAACACGTCCTTG	CAAGGACGTGTTTGCGTTGGCTCG
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241	ATTCGACCGGAAATGAGGTCTTCG	CGAAGACCTCATTTCCGGTCAAT
242	TTGCTTGCTGAGTTGCTCTGTTT	GAACAGAGCAACTCAGCAAGCGAA

	243	CGCGTGAAGACCCCATTCGCCGAGT	ACTCGGGAATGGGGTCTTCACGCG
	244	AACCGTATTCGCGGTCACTTGTGG	CCACAAGTGACCGCGAATACGGTT
	245	GGGGCCAACCGTTTCGAGGCGTAT	ATACGCCTCGAAACGGTTGGCCCC
5	246	TTCGGCTGGCAGTCCAAACGGCTT	AAGCCGTTTGGACTGCCAGCCGAA
	247	GGGTGTGGTTAGAATGCACGGTTC	GAACCGTGCATTCTAACCACACCC
	248	GCGAGGACCGAACTAGACAAACGG	CCGTTTGTCTAGTTCGGTCCTCGC
	249	ACGCACGCGTGACCGAAGTTGCTG	CAGCAACTTCGGTCACGCGTGCGT
	250	TAAAAGGTCGCTTTGAAAGGGGGA	TCCCCCTTTCAAAGCGACCTTTTA
10	251	TGCGATCGCTAACTGCTGGGACAA	TTGTCCCAGCAGTTAGCGATCGCA
	252	GGAGGTATAAGCGGAGCGGCCTCA	TGAGGCCGCTCCGCTTATACCTCC
	253	ATGCTGACATGTCGTGCACCTCGT	ACGAGGTGCACGACATGTCAGCAT
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	255	CGTTCACACCGGCGTAAGCTGCGT	ACGCAGCTTACGCCGGTGTGAACG
15	256	CCTATCCCGGCGAGAACTTCTGTG	CACAGAAGTTCTCGCCGGGATAGG
	257	GTCTGCACTCACGCAGCGGAGGGA	TCCCTCCGCTGCGTGAGTGCAGAC
	258	GCACGAGTTGGTGCTCGGCAGATT	AATCTGCCGAGCACCAACTCGTGC
	259	AACGTCGCACGACACACGTTTCGTC	GACGAACGTGTGTCGTGCGACGTT
	260	ATGCGCGCTTATCCTAGCATGGTC	GACCATGCTAGGATAAGCGCGCAT
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	262	TGTGCCTCATCCTTAGGATACGGC	GCCGTATCCTAAGGATGAGGCACA
	263	AGGTGGTGTGGGTCAACCGCTTTA	TAAAGCGGTTGACCCACACCACCT
	264	CTGGATCGAAGGGACTGCAAGCTC	GAGCTTGCAGTCCCTTCGATCCAG
	265	TAGATCAACTCGCGTACGCATGGA	TCCATGCGTACGCGAGTTGATCTA
25	266	GATCCTGCGGAGAAGAGAGTGACG	CTGCACTCTCTTCTCCGCAGGATC
	267	TACGTGTGGAGATGCCCCGAACCG	CGGTTCCGGGCATCTCCACACGTA
	268	GCGCTATGTCAATCGTGGGCGTAG	CTACGCCACGATTGACATAGCGC
	269	AGCGAGGTTTCTAGCGTCGACACC	GGTGTGACGCTAGAAACCTCGCT
	270	ACCCAGGTTTTGCCGTTGTGGAAT	ATTCCACAACGGCAAAACCTGGGT
30	271	CCCTGTAAACGGCTGCGTAGTCTC	GAGACTACGCAGCCGTTAACAGGG
	272	AGGCCGATTTACCCGCCAATTGC	GCAATTGGCGGGTGAAATCGGCCT
	273	GAGCCCTCACTCCTTGCCCTTTGA	TCAAAGGGCAAGGAGTGAGGGCTC
	274	GGGTGGACATCCGCCTCGCAGTCA	TGACTGCGAGGCGGATGTCCACCC
	275	GATGGCTGAGAACCGTGCTACGAT	ATCGTAGCACGGTTCTCAGCCATC
35	276	TCGACGTTAGGAGTGCTGCCAGAA	TTCTGGCAGCACTCCTAACGTCGA
	277	CGAATGGGTCTGGACCTTGATAG	CTATGCAAGGTCCAGACCCATTCTG
	278	GTGCACCAGACATTGAACTCGGA	TCCGAGTTCGAATGTCTGGTGCAC
	279	AGAGGCCCGGTATATCCCATCCAT	ATGGATGGGATATACGGGGCCTCT
	280	AACGCCTGTTTACAGCATCAGCGG	CCGCTGATGCTCTGAACAGGCGTT
40	281	AAGGCTCAACACGCCTATGTGCGC	GCGCACATAGGCGTGTTGAGCCTT
	282	AGTCCGTGTTGCCAGATTGGCTCG	CGAGCCAATCTGGCAACACGGACT
	283	ATGTCCCATGTAAAGACGCGTGTG	CACACGCGTCTTTACATGGGACAT

	284	ATGGAGTCTGCTCACGCCCAAAGG	CCTTTGGGCGTGAGCAGACTCCAT
	285	CGGCCTCCAACAAGGAGCACTAAC	GTTAGTGCTCCTTGTTGGAGGCCG
	286	CAGAGCCGTGGCAACATTGCGAGC	GCTCGCAATGTTGCCACGGCTCTG
	287	TCATTTGAATGAGGTGCGCACCGG	CCGGTGCGCACCTCATTCAAATGA
5	288	GACGTACCGGAAGCGCCGTATAAA	TTTATACGGCGCTTCCGGTACGTC
	289	ATGCGAGCAATGGGATCCGGATTG	GAATCCGGATCCCATTGCTCGCAT
	290	AGAGTGAGGCCTCCCTGACCAGTG	CACTGGTCAGGGAGGCCTCACTCT
	291	CGCACCGTAAGTAGATTTGCCCGC	GCGGGCAAATCTACTTACGGTGCG
	292	TGAACCTTTGAGCACGTCGTGCGC	GCGCACGACGTGCTCAAAGGTTCA
10	293	TCCGCCTTTTGGTTACCTCGAAG	CTTCGAGGTAACCAAAAAGGCGGA
	294	GAACGCCAACGGCACTAACACATC	GATGTGTTAGTGCCGTTGGCGTTC
	295	CCGACAGCAGCCAAGACGTCCCAG	CTGGGACGTCTTGGCTGCTGTCGG
	296	CATAAAAAACCTGGGGCTCTGCG	CGCAGAGCCCCAGGTTTTTTTATG
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	299	GGGATGCGTATTTTAGCGAACACG	CGTGTTGCTAAAATACGCATCCC
	300	TGGGATTCAGCGACCAGTACGCGA	TCGCGTACTGGTCGCTGAATCCCA
	301	CCCGATATTCGCCCGGCCTATTCG	CGAATAGGCCGGGCGAATATCGGG
	302	CGAGAAGATGCCTCACGCAACCAA	TTGGTTGCGTGAGGCATCTTCTCG
20	303	AACCTTGACCCGTGGATGACGCTA	TAGCGTCATCCACGGGTCAAGGTT
	304	GGCTAGACGATGGATACCCGTGCC	GGCACGGGTATCCATCGTCTAGCC
	305	GCCTCTTCTCGACGATGCGATTTT	AAAATCGCATCGTCGAGAAGAGGC
	306	GCTTCCGGATGAACGGGATGTTTG	CAACCATCCCGTTCATCCGGAAGC
	307	CCCTCCATGTTCTTCGAACGGTTT	AAACCGTTCAAGAACATGGAGGG
25	308	TTGATGGGCGGCAATGCTCTTGCT	AGCAAGAGCATTGCCGCCCATCAA
	309	ATTGTGAGATGCGCCAAATCCCC	GGGGAATTTGGCGCATCTCACAAT
	310	TCAGCACAGCCAGACGGTCAACTT	AAGTTGACCGTCTGGCTGTGCTGA
	311	ACTCCACTCCTCGGTGGCAAACCTA	TAGTTTGCCACCGAGGAGTGGAGT
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	315	AGACAGCGATCCGCGGCTCATGAT	ATCATGAGCCGCGGATCGCTGTCT
	316	CGCGTCTCTAACTGAGAGCAGCCA	TGGCTGCTCTCAGTTAGAGACGCG
	317	AGGCGCACATGTACGGACATTGAG	CTGAATGTCCGTACATGTGCGCCT
35	318	GATGAGTGGCACGTCCGGTGTGTAA	TTACACACCGACGTGCCACTCATC
	319	TGATCCATATTGTCGGACGTTGCG	CGCAACGTCCGACAATATGGATCA
	320	ACCTGCCGGGAGTTCATAGGCTAG	CTAGCCTATGAACTCCCGGCAGGT
	321	AGCATTGGCGTTTTTCCGCAACGA	TCGTTGCGGAAAAACGCCAATGCT
	322	GGTAATATTCAGCGCGACCGCTCA	TGAGCGGTGCGGCTGAATATTACC
40	323	ATAGCGTACGACGAGGTGACGCGC	GCGCGTCACCTCGTCGTACGCTAT
	324	TAGGTCACGATGCGTTTGACGCTA	TAGCGTCAAACGCATCGTGACCTA

	325	ACTGCCCGTACCTCTGGTTCTGGC	GCCAGAACCAGAGGTACGGGCAGT
	326	CCTTTGGCCTGAAGTTGTCGTAGC	GCTACGACAACCTCAGGCCAAAGG
	327	GTGCCCCACGAGCGTATCGTTGTA	TACAACGATACGCTCGTGGGGCAC
	328	AGGCGCTACGTGGGCCTGGAGCAA	TTGCTCCAGGCCACGTAGCGCCT
5	329	GGGTGCTACCATTGCATTAGTCCG	CGGACTAATGCAATGGTAGCACCC
	330	ACCACGCGCGTACGTGTAACCGAG	CTCGGTTACACGTACGCGCGTGGT
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	333	CCGTGTGGCTGGAGATTCGTGTGA	TCACACGAATCTCCAGCCACACGG
10	334	GTTAGGGCGACGCATATTGGCACA	TGTGCCAATATGCGTCGCCCTAAC
	335	GGGTCAGTCAGGTGCGTTAGGATC	GATCCTAACGCACCTGACTGACCC
	336	GCCGTGAAGTCAATGCAGATCGA	TCGATCTGCATTGACTTCACGGC
	337	GCCACCACCCAGTGCATTACAGGTA	TACCTGAATGCACTGGGTGGTGGC
	338	GAGCTTAGTTTGCGGTCATCGGGC	GCCCGATGACCGCAAACCTAAGCTC
15	339	TGTTTGCCGCCATTAGGGAGTAAC	GTTACTCCCTAATGGCGGCAAACA
	340	GCTCCGCTGGATGTGCCGTTTAG	CTAAACCGGCACATCCAGCGGAGC
	341	CGGTAGCATGCGAGATCCCTGTTA	TAACAGGGATCTCGCATGCTACCG
	342	CTACGCTCTACCAGTTGCCTGCGA	TCGCAGGCAACTGGTAGAGCGTAG
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20	344	TTGCGACTCGACTTGACGAGTAG	CTACTCGTCCAAGTCGAGTCGCAA
	345	TCTGGGAGCTGTTTACTCCAGCCA	TGGCTGGAGTAAACAGCTCCCAGA
	346	TGCACGCGGAACTCCCTTTACCAT	ATGGTAAAGGGAGTTCCGCGTGCA
	347	TGGCAGCAAATGAATCGAAAGCAC	GTGCTTTCGATTCAATTGCTGCCA
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25	349	AGACGATTACGCTGGACGCCGTCG	CGACGGCGTCCAGCGTAATCGTCT
	350	ATGCCCTCCTTCATGGAAAGGGTT	AACCCTTTCCATGAAGGAGGGCAT
	351	ATTCTCGGAGCGTATGCGCCAGAA	TTCTGGCGCATACGCTCCGAGAAT
	352	ATAGCGGAGTTTGGGTACGCGAAC	GTTGCGGTACCCAACTCCGCTAT
	353	ACCTACGCATACCGCTTGCGCAGG	CCTCGCCAAGCGGTATGCGTAGGT
30	354	GATTACCTGAATGGCCAAGCGAGC	GCTCGCTTGCCATTGAGGTAATC
	355	CCTGTTAGCATCACGGCGCTTAGG	CCTAAGCGCCGTGATGCTAACAGG
	356	CGGAATGATGCGCTCGACAACGCT	AGCGTTGTCGAGCGCATATTCCG
	357	TGAGAGAGGCGTTGGTTAAGGCAA	TTGCCTTAACCAACGCCTCTCTCA
	358	AAGCAGGCGAAGGGATACTCCTCG	CGAGGAGTATCCCTTCGCCTGCTT
35	359	TCACGACAGACGGGCCGAGATTAC	GTAATCTCGGCCCGTCTGTCGTGA
	360	AAGCAATTTGGCCTCGTTTTGTGA	TCACAAAACGAGGCCAAATTGCTT
	361	GCTGGTTGCGGTAGGATCGCATAT	ATATGCGATCCTACCGCAACCAGC
	362	TTGTGAATCCGTTCTGTCCCCGAC	GTCGGGGACAGAACGGATTACAA
	363	TGGGCTCCTCTGAGGCGAGATGGC	GCCATCTCGCCTCAGAGGAGCCCA
40	364	GGATAGAGTGAATCGACCGGCAAC	GTTGCCGGTCGATTCACTCTATCC
	365	TGCACCGAACGTGCACGAGTAATT	AATTACTCGTGACGTTCCGGTGCA



366	GCCAGTATTCTCGGGTGTGGACG	CGTCCAACACCCGAGAATACTGGC
367	TCGCTACCTAAGACCGGGCCATAC	GTATGGCCCGGTCTTAGGTAGCGA
368	TGGCATTGACGAGCAGCAGTCAGT	ACTGACTGCTGCTCGTCAATGCCA
369	CGCGTCCCAGCGCCCTTGGAGTAT	ATACTCCAAGGGCGCTGGGACGCG
370	ATGAAGCCTACCGGGCGACTTCGT	ACGAAGTCGCCCCGTAGGCTTCAT
371	CCAGACAGATGGCCTGGAACCATG	CATGGTTCCAGGCCATCTGTCTGG
372	TGGCGTGGGACCATCTCAAAGCTA	TAGCTTTGAGATGGTCCCACGCCA
373	CCGCATGGGAACACGTGTCAAGGT	ACCTTGACACGTGTTCCCATGCGG
374	GCCCACTCGTCAGCTGGACGTAAT	ATTACGTCCAGCTGACGAGTGGGC
375	ATTACGGTCTGTATCCAGAAAGCG	CGCTTTCTGGATCACGACCGTAAT
376	TGCGAGGTGAGCACCTACGAGAGA	TCTCTCGTAGGTGCTCACCTCGCA
377	GGGCCGCATTCTTGATGTCCATT	GAATGGACATCAAGAATGCGGCCC
378	CCTCGGATGTGGGCTCTCGCCTAG	CTAGGCGAGAGCCCACATCCGAGG
379	TAGGCATGTTGGCGTGAGCGCTAT	ATAGCGCTCACGCCAACATGCCTA
380	CGATACGAACGAGGATGTCCGCCT	AGGCGGACATCCTCGTTCGTATCG
381	TACGCCGGTTAGCACGGTGCGCTA	TAGCGCACCGTGCTAACC GGCGTA
382	CATACGATGTCCGGGCCGTGTGCG	GCGACACGGCCCGGACATCGTATG
383	ATCCGCAGTTGTATGGCGCGTTAT	ATAACGCGCCATACAAGTGGGAT
384	GGGTAAGGGACAAAGATGGGATGG	CCATCCCATCTTTGTCCCTTACCC
385	ATTGGAGTGTTTTGGTGAATCCGC	GCGGATTACCAAAACACTCCAAT
386	GAACCGAGCCAACGTATGGACACG	CGTGTCCATACGTTGGCTCGGTT
387	GCCGTCAAGCTTAAGGTTTGGGC	GCCCAAACCTTAAGCTTGACGGC
388	ACCTGCTTTTGGGTGGGTGATATG	CATATCACCCACCCAAAAGCAGGT
389	AATCGTGGGCGCAGCAAACGTATA	TATACGTTTGCTGCGCCACGATT
390	GTCGCCGGATTGCTCAGTATAAGC	GCTTATACTGAGCAATCCGGCGAC
391	ACCCGTCGATGCTTCCTCCTCAGA	TCTGAGGAGGAAGCATCGACGGGT
392	ATCCGGGTGGGCGATACAAGAGAT	ATCTCTTGATCGCCACCCGGAT
393	TTCCGCATGAGTCAGCTTTGAAAA	TTTTCAAAGCTGACTCATGCGGAA
394	GCAAAGTCCCACTGGCAAGCCGAT	ATCGGCTTGCCAGTGGGACTTTGC
395	CGACCTCGGCTTCATCGTACACAT	ATGTGTACGATGAAGCCGAGGTG
396	CTCATGAGCGCAGTTGTGCGTGAG	CTCACGCACAAGTGCCTCATGAG
397	CAGATGAAGGATCCACGGCCGGAG	CTCCGGCCGTGGATCCTTCATCTG
398	TCAAAGGCTCTTGATACAGCCGT	ACGGCTGTATCCAAGAGCCTTTGA
399	TCCGCTAATTTCCAATCAGGGCTC	GAGCCCTGATTGGAAATTAGCGGA
400	ACGCACGGCGCTTTTGCCCTAATG	CATTAAGGCAAAAGCGCCGTGCGT
401	TGACAACGTCAACAAGGAGCAGGAC	GTCCTGCTCCTTGACGTTGTCA
402	CTTAGTTGGGGCGCGGTATCCAGA	TCTGGATACCGCGCCCCAACTAAG
403	GCTCTAATGCCGTGGAGTCGGAAC	GTTCCGACTCCACGGCATTAGAGC
404	CCGATTACAAATTGACTGACCGCA	TGCGGTGAGTCAATTTGTAATCGG
405	AGACGTACGTGAGCCTCCCGTGTC	GACACGGGAGGCTCACGTACGTCT
406	AATGGAGCGATACGATCCAACGCA	TGCGTTGGATCGTATCGCTCCATT

	407	GGAGGCGCTGTACTGATAGGCGTA	TACGCCTATCAGTACAGCGCCTCC
	408	TGTTTTTGAATTGACCACACGGGA	TCCCGTGTGGTCAATTCAAAAACA
	409	CATGTCTGGATGCGCTCAATGAAG	CTTCATTGAGCGCATCCAGACATG
5	410	GCCCGCTAATCCGACACCCAGTTT	AAACTGGGTGTCTGGATTAGCGGGC
	411	CCATTGACAGGAGAGCCATGAGCC	GGCTCATGGCTCTCCTGTCAATGG
	412	GAATCACCGAATCACCGACTCGTT	AACGAGTCGGTGATTCTGGTGATTC
	413	AACCAGCCGCGAGTAGCTTACGTCG	CGACGTAAGCTACTGCGGCTGGTT
	414	TTTTCTGAGGGACACGCGGGCGTT	AACGCCCGCGTGTCCCTCAGAAAA
	415	GGTGCTCCGTTTGATCGATCCTCC	GGAGGATCGATCAAACGGAGCACC
10	416	CCGCTTAGGCCATACTCTGAGCCA	TGGCTCAGAGTATGGCCTAAGCGG
	417	TAAGACATACCGACGCCCTTGCCT	AGGCAAGGGCGTCGGTATGTCTTA
	418	GTTCCCGACGCCAGTCATTGAGAC	GTCTCAATGACTGGCGTCGGGAAC
	419	TAAAAGTTTCGCGGAGGTCGGGCT	AGCCCGACCTCCGCGAAACTTTTA
	420	CGGTCCAGACGAGCTGAGTTCGGC	GCCGAACCTCAGCTCGTCTGGACCG
15	421	CGGCGTAGCGGCTACGGACTTAAA	TTTAAGTCCGTAGCCGCTACGCCG
	422	GCTTGATGCCCATGCGGCAAGGT	ACCTTGCCGCATGGGCATCCAAGC
	423	AGCGGGATCCCAGAGTTTCGAAAA	TTTTCGAAACTCTGGGATCCCGCT
	424	GAGCTTGAGAGCGAGGTCATCCTC	GAGGATGACCTCGCTCTCAAGCTC
	425	GCATCGGCCGTTTTGACCATATTC	GAATATGGTCAAACGGCCGATGC
20	426	CATAGCGCTGCACGTTTCGACCGC	GCGGTCGAAACGTGCAGCGCTATG
	427	ACCCGACAACCACCAATTCAAAAA	TTTTTGAATTGGTGGTTGTCTGGGT
	428	GCGAACACTCATAAGAGCGCCCTG	CAGGGCGCTCTTATGAGTGTTTCGC
	429	CCGCCGAGTGTAGAGAGACTCCGA	TCGGAGTCTCTCTACACTCGGCGG
	430	GACATCGGGAGCCGGAACATGAG	CTCATGTTTCCGGCTCCCGATGTC
25	431	TCGTGTAGACTCGGCGACAGGCGT	ACGCCTGTGCGCGAGTCTACACGA
	432	ATGCGCATATACTGACTGCGCAGG	CCTGCGCAGTCAGTATATGCGCAT
	433	ACAAGCGAACCCGAGTTTTGATGA	TCATCAAAACTCGGGTTCGCTTGT
	434	GCATGAGACTCCGCGAAGACATGT	ACATGTCTTCGCGGAGTCTCATGC
	435	TCCTACATGTGCGGTACGATCAC	GTGATCGTGACGCGACATGTAGGA
30	436	GACCGATCGCGAAGTCGTACACAT	ATGTGTACGACTTCGCGATCGGTC
	437	GTCGCCAGGACTGGGCCGATGTGA	TCACATCGGCCAGTCTTGCGGAC
	438	ACCGATAAGACTTGCATCCGAACG	CGTTCGGATGCAAGTCTTATCGGT
	439	TCCATAACCAGTCCGAAGTGCCGG	CCGGCACTTCGGACTGGTTATGGA
	440	ACGCGCCCTGCATCTCGTATTTAA	TTAAATACGAGATGCAGGGCGCGT
35	441	AGACCGCATCAATTGGCGCGTACC	GGTACGCGCCAATTGATGCGGTCT
	442	AGAGGCTTGGCAAGTAGGGACCCT	AGGGTCCCTACTTGCCAAGCCTCT
	443	GCAATGGACGCCAGACGATACCGG	CCGGTATCGTCTGGCGTCCATTGC
	444	GCTGGACTTAGTCGTGTTTCGGCGG	CCGCCGAACACGACTAAGTCCAGC
	445	AGGCATCGTGCCGGATTGCTCCCT	AGGGAGCAATCCGGCACGATGCCT
40	446	TGCGCATGTGCGACGTTGAACAAAG	CTTTGTTCAACGTCGACATGCGCA
	447	TTCGGGTACATCCGATGCCATAC	GTATGGCATCGGATGTGACCCGAA

448	ACCCATCGCCGGAAAGCGATGTTG	CAACATCGCTTTCCGGCGATGGGT
449	AAGCGCTGACTCGGCTAAGAATCA	TGATTCTTAGCCGAGTCAGCGCTT
450	ACTTCCAAGTCCTTGACCGTCCGA	TCGGACGGTCAAGGACTTGGAAGT
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452	AACAGTTCCTCTTTTTCCTGGCGC	GCGCCAGGAAAAAGAGGAAGTGT
453	CGTCCTCCATGTTGTCACGAACAG	CTGTTCTGTGACAACATGGAGGACG
454	TGCGCAGACCTACCTGTCTTTGCT	AGCAAAGACAGGTAGGTCTGCGCA
455	ATGGACGGCTTCGCAGTCCTCCTT	AAGGAGGACTGCGAAGCCGTCCAT
456	TGAACGCTTTCTATGGGCCACGTA	TACGTGGCCCATAGAAAGCGTTCA
457	TGAACCCTGCCGCGAGCGATAACC	GGTTATCGCTCGCGGCAGGGTTCA
458	GTTCTTGCGCGATGAATCAGGACC	GGTCCTGATTCATCGCGCAAGAAC
459	AGGGTACGTGTGCGAGCTTCGCGT	ACGCGAAGCTGCGACACGTACCCT
460	ACCCTTGCTCCGCCATGTCTCTCA	TGAGAGACATGGCGGAGCAAGGGT
461	GGGACAAGGATTGAAGCTGGCGTC	GACGCCAGCTTCAATCCTTGTCCC
462	TGTCGTTGCTCCCGAGTACCATTG	CAATGGTACTCGGGAGCAACGACA
463	GTTGTCCGAGACGTTTGTGTCAGC	GCTGACACAAACGTCTCGGACAAC
464	GCTGGTGAACACTCACGAACCGCT	AGCGGTTCTGTAGTGTTCAACAGC
465	GCAGACAGGGCAAATCGGTGCAAA	TTTGCACCGATTTGCCCTGTCTGC
466	CCCATCACAACGAGTGGCGACTTT	AAAGTCGCCACTCGTTGTGATGGG
467	GCTTCTACAGCTGGCGTGCTAGCG	CGCTAGCACGCCAGCTGTAGAAGC
468	GAATGTGTGCCGACCATTCTAGCC	GGCTAGAATGGTCGGCACACATTC
469	CCAGCGGAAGTTAGAGCTCTGTGG	CCACAGAGCTCTAACTTCCGCTGG
470	TTTTTACCGACCACTCCATGTCGG	CCGACATGGAGTGGTCGGTAAAAA
471	GCGGCTATGTGATGACGGCCTAGC	GCTAGGCCGTCATCACATAGCCGC
472	AGTACACGGGCGTGTTAGCGCTCC	GGAGCGCTAACACGCCCGTGACT
473	TCCTGTGTGGTGGCGCACTCCAC	GTGGGAGTGCGCCACCACACAGGA
474	CCAACTAACCAATCGCGCGGATGA	TCATCCGCGCGATTGGTTAGTTGG
475	AGTGAGTGACCAAGGCAGGAGCAA	TTGCTCCTGCCTTGGTCACTCACT
476	CATCTTTCGCGGAGTTTATTGCGG	CCGCAATAAACTCCGCGAAAGATG
477	CTTCGTCCGGTTAGTGCGACAGCA	TGCTGTGCGCACTAACC GGACGAAG
478	CTCACGAAAACGTGGGCCCGAAAT	ATTTGCGGCCACGTTTTCTGTGAG
479	CGCAGCAGCTGAACCTTAGCATTG	CAATGCTAGAGTTCAGCTGCTGCG
480	AGGAGACATACGCCCAAATGGTGC	GCACCATTTGGGCGTATGTCTCCT
481	ATTGAGAACTCGTGCGGGAGTTTG	CAAACCTCCGCGACGAGTTCTCAAT
482	CTCTTTGTAGGCCCAGGAGGAGCA	TGCTCCTCCTGGGCCTACAAAGAG
483	GCCGCAGGGTCGATAATTGGTCTA	TAGACCAATTATCGACCCTGCGGC
484	AAACGCCGCCCTGAGACTATTGGG	CCCAATAGTCTCAGGGCGGCGTTT
485	CTGAGTTGCCTGGAACGTTGGACT	AGTCCAACGTTCCAGGCAACTCAG
486	CGGATGGGTTGCAGAGTATGGGAT	ATCCCATACTCTGCAACCCATCCG
487	CTGACCTTTGGGGGTTAGTGCGGT	ACCGCACTAACCCCAAAGGTCAG
488	GGAAATGAGAACCTTACCCACGCG	CGCTGGGGTAAGGTTCTCATTTCC

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490	TGGAGAGAGACTTCGGCCATTGTT	AACAATGGCCGAAGTCTCTCTCCA
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492	AGCGCGTTAAAGCACGGCAACATT	AATGTTGCCGTGCTTTAACGCGCT
493	AGCCAGTAACTGTGGGCGGCTGT	ACAGCCGCCACAGTTTACTGGCT
494	CGACTGATGTGCAACCAGCAGCTG	CAGCTGCTGGTTGCACATCAGTCG
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496	GCGCAAATCCACGGAACCCGTACC	GGTACGGGTTCCGTGGATTGCGC
497	ACGCAGTTTATTCCCCTGGCTTCT	AGAAGCCAGGGGAATAAACTGCGT
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504	CCACCGGTCGCTTAAGATGCACTT	AAGTGCATCTTAAGCGACCGGTGG
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506	AAGCGGAACGGGTTATACCGAGGT	ACCTCGGTATAACCCGTTCCGCTT
507	TGCACACTAGGTCCGTCGCTTGAT	ATCAAGCGACGGACCTAGTGTGCA
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509	GAATTACAACCACCCGCTCGTGTT	AACACGAGCGGGTGGTTGTAATTC
510	TTCAGTGCTCACGAAGCATGGATT	AATCCATGCTTCGTGAGCACTGAA
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512	AATGCGACCTCGACGAGCCTCATA	TATGAGGCTCGTCGAGGTCGCATT
513	CCGAAACCGTTAACGTGGCGCACA	TGTGCGCCACGTTAACGGTTTCGG
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515	TAATGATTTTAGTCGCGGGGTGGG	CCCACCCCGCGACTAAATCATT
516	GGCTACTCTAAGTGCCCGCTCAGG	CCTGAGCGGGCACTTAGAGTAGCC
517	TGGCGGACGACTCAATATCTCACG	CGTGAGATATTGAGTCGTCCGCCA
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519	GCCACCTTTAGACGGCGGCTCTAG	CTAGAGCCGCCGTCTAAAGGTGGC
520	GAGATGTGTAAACGTGCAGGCACC	GGTGCCTGCACGTTTACACATCTC
521	TAGCTCGTGGCCCTCCAAGCGTGT	ACACGCTTGAGGGGCCACGAGCTA
522	GTGTGCGCGCTATTTGGCCTTACC	GGTAAGGCCAAATAGCGCCGACAC
523	CCAGGGAAGCAACTGGTTGCCATT	AATGGCAACCAGTTGCTTCCCTGG
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525	GCAAACCCGGTAACCCGAGAGTTC	GAACCTCTCGGGTTACCGGGTTTGC
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527	AGTACTTTCGCGCCCAGTTTAGGG	CCCTAAACTGGGCGCGAAAGTACT
528	AAGATCTGCGAGGCATCCCGGCTT	AAGCCGGGATGCCTCGCAGATCTT
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543	ATACCTCCGCAGAACCATTCCGTT	AACGGAATGGTTCGCGGAGGTAT
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546	TTATCGCGAGAGACGACCGTGTCC	GGACACGGTCGTCTCTCGCGATAA
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552	CCACCCCGACAGCGCTGGACTCTT	AAGAGTCCAGCGCTGTCGGGGTGG
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554	CATATCAGCGTCGTCTAGCTCGCG	CGCGAGCTAGACGACGCTGATATG
555	TGATCCCGGACCGGCTAGACTAAT	ATTAGTCTAGCCGGTCCGGGATCA
556	GGCCCCGACACTACAGGGTAATCA	TGATTACCCTGTAGTGTCGGGGCC
557	GGCTCCAGGGCGAGATTATGAATG	CATTCATAATCTCGCCCTGGAGCC
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559	CACAGGCGCATAGGGAGCAAGCTA	TAGCTTGCTCCCTATGCGCCTGTG
560	TAGCTATTGCCCCGATGGGCTACT	AGTAGCCCATCGGGGCAATAGCTA
561	TGGTACGCGGTCCATAGCAAGTCG	CGACTTGCTATGGACCGCGTACCA
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563	CCTGGGTTGCGCGCGTGGTAACTG	CAGTTACCACGCGGCGAACCAGG
564	TTCCCGCGTAGCCCAACAGCTATA	TATAGCTGTTGGGCTACGCGGGAA
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569	TGTCCATGACGTCGTTTCTCTGGT	ACCAGAGAAACGACGTCATGGACA
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573	GGTGTCTGGAGGGTGGTGACCTCGA	TCGAGGTCACCACCCTCCGACACC
574	AGCGCTTTTGGTCATGATTGCAA	TTGCAAATCATGACCAAAAGCGCT
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583	CAACATTGTGGTGGCACTCCATCC	GGATGGAGTGCCACCACAATGTTG
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585	GGCTATAAACGTGCGGACTGCTCC	GGAGCAGTCCGCACGTTTATAGCC
586	TGGGTAAATCACTATTGCGCGGTT	AACCGCGCAATAGTGATTACCCA
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591	ACTCCGAAGCTTCGAGCGGCACGA	TCGTGCCGCTCGAAGCTTCGGAGT
592	TCCCGCCCACTAGACTGACTCGTA	TACGAGTCAGTCTAGTGGGCGGGA
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594	ATCATCCCACGGCAGAGTGAAGAG	CTCTTCACTCTGCCGTGGGATGAT
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596	CGGTCTCAGCAACACTGTCGCAA	TTTGCGACAGTGTTGCTGAGACCG
597	CGAACGTTCTCCGATGTAATGGCC	GGCCATTACATCGGAGAACGTTTCG
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	613	ATGCAGATGAACAAATCGCCGAAT	ATTCGGCGATTGTTCATCTGCAT
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	615	AGGGTTCCTTACGCGTCGACATGG	CCATGTGACGCGTAAGGAACCCT
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	617	TCGTAGTCTCACC GGCAATGATCC	GGATCATTGCCGGTGAGACTACGA
	618	TTATAGCAGTGCGCCAATGCTTCG	CGAAGCATTGGCGCACTGCTATAA
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	620	TCCGCGTGGACTGTTAGACGCTAT	ATAGCGTCTAACAGTCCACGCGGA
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	623	CGACTCGCTGGACAGGAGAATCGT	ACGATTCTCCTGTCCAGCGAGTCG
	624	CATGATCCTCTGTTTCACCCGCGG	CCGCGGGTGAAACAGAGGATCATG
	625	GGCGTAGCGCTCTAAAAGCTTCGG	CCGAAGCTTTTAGAGCGCTACGCC
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	628	CTGTGGTTGATGGAGGATCCACAC	GTGTGGATCCTCCATCAACCACAG
	629	ACTCGCTGGAATTTGCGCTGACAC	GTGTCAGCGCAAATTCAGCGAGT
	630	CAGGCCCCGAACCACGCGTTACAG	CTGTAACCGCGTGGTTCGGGCCTG
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	637	TCGTTTCGGCCTTGAGAGTATCG	CGATACTCTCAAGGCCGAAACGA
	638	AGGTGCAAGTGCAAGGCGAGAGGC	GCCTCTCGCCTTGCACTTGACCT
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	640	GCTTTACCGCCGATCCCAGATATC	GATATCTGGGATCGGCGGTAAAGC
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	644	GGCGAGTCTTGTGGGGACATGTGT	ACACATGTCCCCACAAGACTCGCC
	645	CCAAAGCGAAGCGAGCGTGTCTAT	ATAGACACGCTCGCTTCGCTTTGG
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	648	GGCTTCGCACCCGTACCAATTTAG	CTAAATTGGTACGGGTGCGAAGCC
	649	TGTAGAGTCCCACGTAGCCGGCAT	ATGCCGGCTACGTGGGACTCTACA
	650	CACTAGTCTGGGGCAAGGTGCATT	AATGCACCTTGCCCCAGACTAGTG
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	655	ATGCATCGAACTAGTCGTGACGGC	GCCGTCACGACTAGTTCGATGCAT
	656	TTCCAGGCATTAAGGAGAGGGAGC	GCTCCCTCTCCTTAATGCCTGGAA
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	658	CTCATCGTCCTAACACGAGAGCCC	GGGCTCTCGTGTTAGGACGATGAG
	659	AATGGCACTTCGGCGGTGATGCAA	TTGCATCACCGCCGAAGTGCCATT
	660	CCGTGGGAGGGAATCCAACCGAGG	CCTCGGTTGGATTCCCTCCACGG
	661	AAATTCTCGTTGGTGACGGCTCAT	ATGAGCCGTACCAACGAGAATTT
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	664	CGCGACTAAGGTGCTGCAACTCGA	TCGAGTTGCAGCACCTTAGTCGCG
	665	GCTCGATTTACGCGCCCGTTGTTT	GAACAACGGGCCGTGAAATCGAGC
	666	AGCAGAGTGCGTTGCAGAGGCTAA	TTAGCCTCTGCAACGCACTCTGCT
15	667	TGGAGGTGAGGACGACGTGCACTA	TAGTGACGTCGTCTCACCTCCA
	668	AACCGTTTAGGGTACATTGCGGGT	ACCGCGAATGTACCCTAAACGGTT
	669	TATGATCGCTCGGCTCACAGTTTG	CAAACGTGAGCCGAGCGATCATA
	670	GACTTTTTGCGGAAACGTCATGGT	ACCATGACGTTTCCGCAAAAAGTC
	671	TGTCGGTTATTCCACCTGCAAGGA	TCCTTGCAGGTGGAATAACCGACA
20	672	CTATGGTTTGCACTGCGCCGTCGA	TCGACGGCGCAGTGCAAACCATAG
	673	AGCAGGGAAATTCAATCGTTTCGCA	TGCGAACGATTGAATTTCCCTGCT
	674	CCTAACCGAGCGCTTAGCATTTC	GGAAATGCTAAGCGCTCGGTTAGG
	675	CCCGACCCTAACTCGCATTGAATA	TATTCAATGCGAGTTAGGGTCGGG
	676	TTGCTTAATGGTGACGCCACGGAT	ATCCGTGGCGTCACCATTAAGCAA
25	677	GATGCTCGCCGTGTTTAGTTCACG	CGTGAACATAACACGGCGAGCATC
	678	TCGGATGACGAGTTTCCATGACGG	CCGTCATGGAACTCGTCATCCGA
	679	ATGCGGTCTACTTTCTCGATCGGG	CCCGATCGAGAAAGTAGACCGCAT
	680	TTGCGAGGCTAAGCACACGGTAAA	TTTACCGTGTGCTTAGCCTCGCAA
	681	AACTTAATTACCGCCTCTGGCGCC	GGCGCCAGAGGCGGTAATTAAGTT
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	683	TGCGGATTACCGATTGCTCTTAA	TTAAGAGCGAATCGGTAATCCGCA
	684	TGATAGGGGGCCACGTTGATCAGA	TCTGATCAACGTGGCCCCCTATCA
	685	TCGCTCCGTAGCGATTATCGTAG	CTACGATGAATCGCTACGGAGCGA
	686	TGTCAGCTGGTAGCCTCCGTTTGA	TCAAACGGAGGCTACCAGCTGACA
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	688	TCACTCAGCGCTGTGACTGCCTGA	TCAGGCAGTCACAGCGCTGAGTGA
	689	GTTTGCGCTATAGTGGGGGACCGT	ACGGTCCCCCACTATAGCGCAAAC
	690	GTCGCATTCTGCACTGGCTTCGCC	GGCGAAGCCAGTGACAGTATGCGAC
	691	TGATTAGGTGCGGTCCCGTAGTCC	GGACTACGGGACCGCACCTAATCA
40	692	AAGGGACCTTGGGTGACGGCGAGA	TCTCGCCGTACCCAAGGTCCCTT
	693	TCAAATGGCCACCGCGTGTCAATC	GAATGACACGCGGTGGCCATTTGA



694	CTCCGACGACCAATAAATAGCCGC	GCGGCTATTTATTGGTCGTCGGAG
695	GGCTATTCCCGTAGAGAGCGTCCA	TGGACGCTCTCTACGGAATAGCC
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705	TTTAGTCGGACCCTGTGGCAATTC	GAATTGCCACAGGGTCCGACTAAA
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710	TACGTCGGATCCATTGCGCCGAGT	ACTCGGCGCAATGGATCCGACGTA
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712	AGCCAGGCGCGTATATACGCTCGG	CCGAGCGTATATACGCGCCTGGCT
713	ATTTGGCACGTGTCGTGCCATGTT	AACATGGCACGACACGTGCCAAAT
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715	TTGGACGTGACAAGCATGGCGCTC	GAGCGCCATGCTTGTACGTCCAA
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718	CTAACAAATTGCCAACCGGGACGGC	GCCGTCCCGGTTGGCAATTGTTAG
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722	AGGCGATAGCATGGTCCCATATGA	TCATATGGGACCATGCTATCGCCT
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724	AGTAGTGGTCTCCAGATCGGCAA	TTGCCGATCTGGAGGACCACTACT
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729	CAAGGCGAGTCCACTCGAGGGGAC	GTCCCCTCGAGTGGACTCGCCTTG
730	GCAACTTGACGCGCATAAGTGGCC	GGCCAATTATGCCGTGCAAGTTGC
731	TCCGAGCTTGACGTTGCGGACGTC	GACGTCGCGAACGTCAAGCTCGGA
732	AGCGCTGGGCTGTGCTGCCATCTC	GAGATGGCAGCACAGCCCAGCGCT
733	TTCATGTCGCTGAGTAACCCTCGC	GCGAGGGTTACTCAGCGACATGAA
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	735	CACGGAAGGTGGGACAAATCGCCG	CGGCGATTGTCCCACCTTCCGTG
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	737	TTTTCGCAACTCGCTCCATAACCC	GGGTTATGGAGCGAGTTGCGAAAA
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	740	CTTCCACAATTGTCTGCGACGCAC	GTGCGTCGCAGACAATTGTGGAAG
	741	TGCACAAAGGTATGGCTGTCCGGC	GCCGGACAGCCATACCTTTGTGCA
	742	TCCGATGCCAGTCCCATCTTAAGA	TCTTAAGATGGGACTGGCATCGGA
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	745	TCTAGCAGGCCTTTTGAATCGCCA	TGGCGATTCAAAGGCCTGCTAGA
	746	GAGTCACCTCTGAGACGGACGCCA	TGGCGTCCGTCTCAGAGGTGACTC
	747	TCTTCTGTCATCCTGCAGCAGCAT	ATGCTGCTGCAGGATGACAGAAGA
	748	GCGGATGAAACCTGAAAGGGGCCT	AGGCCCTTTCAGGTTTCATCCGC
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	750	GCATTGGCTTCGATTCTCCTACA	TGTAGGAGAATCCGAAGCCAATGC
	751	AGGCGGCCCAACTGTGAGGTCTTG	CAAGACCTCACAGTTGGGCGCCT
	752	ACACCATGTGCTCCGCGCTGCAGT	ACTGCAGCGCGGAGCACATGGTGT
	753	ACGATGAACATGAATCGGGAGTCG	CGACTCCCGATTTCATGTTTCATCGT
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	755	GTGCCGTATTTGACCTGTGCGTT	AACGCACAGGTCGAAATACGGCAC
	756	GCAGTGCGCACTTCAGTTCAAAG	CTTTTGAAGTGAAGTGCACACTGC
	757	GCGATTTTAAGCGATGCCTTGACG	CGTCAAGGCATCGCTTAAATCGC
	758	TAGGTGACCTAGGCTTGCTTGCGG	CCGCAAGCAAGCCTAGGTCACCTA
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	760	CCCCTTACGGCTCGTCGTCTATGC	GCATAGACGACGAGCCGTAAGGGG
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	762	TTTCTGTAAGCGGCCTGGGGTTCA	TGAACCCAGGCCGCTTACAGAAA
	763	GGCTGAGGTGAGCGGTAAGGATGA	TCATCCTTACCGCTCACCTCAGCC
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	766	GTAATCCATTTGTGGCTGCGTCAA	TTGACGCAGCCACAAATGGATTAC
	767	CAAACCCATTCCAGCAGACGCCTG	CAGGCGTCTGCTGGAATGGGTTTG
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	770	GCAAGTGCTTAGCTCGTCAGCCTC	GAGGCTGACGAGCTAAGCACTTGC
	771	CTGGCTGTGTCGCATCTCGTTAAC	GTTAACGAGATGCGACACAGCCAG
	772	CTAACGTCGTCTCGCGCAATCACT	AGTGATTGCGCGAGACGACGTTAG
	773	TTTTCATAAACGTTGTCCCCGAGC	GCTCGGGGACAACGTTTATGAAAA
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	775	TTCAAGCACCATCGTGCAATCCAA	TTGGATTGCACGATGGTGCTTGAA

	776	AGCGTCGCCAGTGATCGCTAGTGG	CCACTAGCGATCACTGGCGACGCT
	777	TACATTCCCTGCCTCCGTGGGCTT	AAGCCACGAGGCAGGGAATGTA
	778	CGCTTCGCGTATTCAGTAGCGGT	AACCGCTACTGAATACGCGAAGCG
5	779	TCGGACGCGTCGACACTCATTATA	TATAATGAGTGTGACGCGTCCGA
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	783	GTTTCATAGGCCACGCGTGCTAAA	TTAGCACGCGTGGCCTATGAAAC
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	785	ATTGGCCGAGGGTGAATGCAGCCT	AGGCTGCATTACCCCTCGGCCAAT
	786	TGATCCATCCGAATGCTTTTCCAT	ATGGAAAAGCATTCGGATGGATCA
	787	GCACACAGTTGTCTTGCCCATGA	TCATGGGCCAAGACAACGTGTGTC
	788	CTGGCGGGCAGTGGAAAAACAAC	GTTGTTTTTCCACTGCCCGCCAG
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	791	TAGCGTATTCACCTTTGCCGAGCA	TGCTCGGCAAGAGTGAATACGCTA
	792	CAATCAAAGCCACGGCGCGATGG	CCATCGCGCCGTGGCTTTTGATTG
	793	AGCGTCACGGAATTCAGCAGATCT	AGATCTGCTGAATTCCGTGACGCT
	794	GACTCCCTGTAAATGCGCCCAAGG	CCTTGGGCGCATTAAACAGGGAGTC
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	797	CGTGCGTACCATGTGTAAGTGCGT	ACGCACTTACACATGGTACGCACG
	798	GACCAATTCTACTTCGGCAGCCCA	TGGGCTGCCGAAGTAGAATTGGTC
	799	ATCGGACCGATTGCTTTTGCGTG	CAGCCAAAAGCAAATCGGTCCGAT
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	802	TGGCGACTACTGTTCCCCTGAATC	GATTCAGGGGAACAGTAGTCGCCA
	803	CAGAGGGGACAGCCGTATGCCTTA	TAAGGCATACGGCTGTCCCCTCTG
	804	CGGTGGTTTTATCGGAATCTGCGA	TCGCAGATTCCGATAAAACCACCG
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	806	CGTTTCGCTAGCATCTGGCGCCGA	TCGGCGCCAGATGCTAGCGAAACG
	807	ACTAAGCGGTGGAGCCGGTGGATG	CATCCACCGGCTCCACCGCTTAGT
	808	ATATTGGCTGCGTTTACGGGCCGC	GCGGCCCGTAAACGCAGCCAATAT
	809	CCGCTATGGTGGCAATCCCGATAC	GTATCGGGATTGCCACCATAGCGG
35	810	GTTGCATGTGGCTCAGGCGGCATA	TATGCCGCCTGAGCCACATGCAAC
	811	ATTCTGGGGAGTGACCCAGGGCTT	AAGCCCTGGGTCACTCCCCAGAAT
	812	CTCTCCAAGGAGACGAGCCAATGT	ACATTGGCTCGTCTCCTTGGAGAG
	813	GAAAGGACGGGATTTGGGGGCTAA	TTAGCCCCCAAATCCCGTCCTTTC
	814	TATGTAGTACCTTGGCTCGCGCCA	TGGCGCGAGCCAAGGTACTACATA
40	815	TCCCTTTCGATGAGCGGCTGTACT	AGTACAGCCGCTCATCGAAAGGGA
	816	TAGATCGGGCAGAGCCGTATCTT	AAGATACGGGCTCTGCCCGATCTA

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817	GGAATGCTTTAGGCTGCCGAGCTG	CAGCTCGGCAGCCTAAAGCATTCC
818	ATGGTAGCAACATTCAACGCCAGG	CCTGGCGTTGAATGTTGCTACCAT
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842	GAATTTGGAACGGTGTTCCGATGA	TCATCGGAACACCGTTCCAAATTC
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	874	AAATGCGATCGCCCTTATGGAAT	ATTCCATAAGGGGCGATCGCATTT
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	896	TACCTCGAGTGCCGTTGATCGGG	CCCGATCAACGGCCACTCGAGGTA
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899	GTGGGCGTGAGTGACACGCACAAA	TTTGTGCGTGCTCACTCACGCCAC
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901	TGTGGTCATGGCGCTACTGTTTTC	GAAAACAGTAGCGCCATGACCACA
902	CTTTCGCTAGCCAGAGCGGGTTC	GGAACCCGCTCTGGCTAGCGAAAG
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904	GGTACTTCCGGCGTATCGGGCCAC	GTGGCCCGATACGCCGGAAGTACC
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906	ACGCAATTCGCATTACTTACCCG	CGGGTAAGTAATGCGGAATTGCGT
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908	GTGAAATGGATCCAGAGAGGGCCA	TGGCCCTCTCTGGATCCATTTCAC
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922	CGCTTAACGGCATTGACTGTCCAC	GTGGACAGTCAATGCCGTTAAGCG
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924	TTTATGCCGTTGCCGAGGAAGACT	AGTCTTCCTCGGCAACGGCATAAA
925	AGTGCCGAGATAGGGGACTGGGCG	CGCCCAGTCCCCTATCTCGGCACT
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927	CCGCCATTCCGAAGATGGATGATG	CATCATCCATCTTCCGAATGGCGG
928	TGACGGTGAAAGTCGATTGCGAAG	CTTCGCAATCGACTTTCACCGTCA
929	ATATGCGTCACCACCCGGTTCCGA	TCGGAACCGGGTGGTGACGCATAT
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932	TCTGCTTTGGAAGCCTGAACTGCT	AGCAGTTCAGGCTTCCAAAGCAGA
933	CGATTTGGTCAAGAAGGCGGAAAT	ATTTCCGCCTTCTTGACCAAATCG
934	ATCAGAGGCCTTCCCGCCTCGTTA	TAACGAGGCGGGAAGGCCTCTGAT
935	ATTGTTGTGCTTGCCACATCGCAG	CTGCGATGTGGCAACGACAACAAT
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942	GCTTGAACCTCGAGGCGATGTTCT	AGAACATCGCCTCGAGGTTCAAGC
943	CAAGCGTGGAAGTACGACCCGCCA	TGGCGGGTCGTACTTCCACGCTTG
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945	TCCCTGGGCTAGCATTGCGAGGTT	AACCTCGCAATGCTAGCCAGGGA
946	AGAACCAAAGACGCTTGTTTGCCG	CGGCAAACAAGCGTCTTTGGTTCT
947	CGTCACATGCAAACGTTCCCTCCC	GGGAGGGAACGTTTGCATGTGACG
948	TGACCGCATGTGTATTGAGTCGCT	AGCGACTCAATACACATGCGGTCA
949	GCGGGCCCAATGAGTATCCGTCAT	ATGACGGATACTCATTGGGCCCGC
950	TAGTGACTGTGAACGCCCTGGTT	AACCAGGGGCGTTCACAGTCACTA
951	GGCACCGTCTGCCGCGCGTATATC	GATATACGCGCGGCAGACGGTGCC
952	TCGATGCAGTCTTTTTCCCGTCAA	TTGACGGGAAAAAGACTGCATCGA
953	ACCCCGTGGGGTTTCGCCATTTT	AAAAATGGCGAAACCCACGGGGT
954	CTACACGCGCAGTTGTGACTTGTG	CACAAGTCACAACTGCGCGTGTAG
955	CGCAGCGACCTCATCTCTGGAGCC	GGCTCCAGAGATGAGGTCGCTGCG
956	CGACCCAGCACTCCTAAAATCGGT	ACCGATTTTAGGAGTGCTGGGTGCG
957	ACGCGCCGCTCATCACTACAATCT	AGATTGTAGTGATGAGCGGCGCGT
958	CGCAACTTCCTGTGGCAAAGCCAG	CTGGCTTTGCCACAGGAAGTTGCG
959	TCGTTGGGCACATAAGGCAACTGA	TCAGTTGCCTTATGTGCCCAACGA
960	CCGCTTGTAATTGCCATTCTCCGT	ACGGAGAATGGCAATTACAAGCGG
961	GTAACCAGGGAGTCCTGGGCTGTG	CACAGCCCAGGACTCCCTGGTTAC
962	AGCGCAAGATCTGGGGGCAGTCAC	GTGACTGCCCCCAGATCTTGCGCT
963	GCGTACATCTGCTCATCAGCATGG	CCATGCTGATGAGCAGATGTACGC
964	CCTCTGTGGCAGGAAAGAAACCGT	ACGGTTTCTTTCCTGCCACAGAGG
965	CCTATGCAATGGACCTGCATCGGA	TCCGATGCAGGTCCATTGCATAGG
966	CTCGGTGGATGGCGAATAAGGATA	TATCCTTATTGCGCATCCACCGAG
967	CCTCACTCGTGATGGCGTGACGCA	TGCGTCACGCCATCACGAGTGAGG
968	TACGCTCACAGAACGCCATACGCC	GGCGTATGGCGTTCTGTGAGCGTA
969	CCGGAGAAGTTACGCGGATCGGAC	GTCCGATCCGCGTAACCTCTCCGG
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971	ACTTTCAGCACGCGAACAGCGCAA	TTGCGCTGTTGCGGTGCTGAAAGT
972	CTAAACGCCCTTGATGCATGAGCA	TGCTCATGCATCAAGGGCGTTTAG
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974	CAGACATCGTACGCACTCGGCATC	GATGCCGAGTGCGTACGATGTCTG
975	TAGCCGCGCGGCTCCTATGCTCTT	AAGAGCATAGGAGCCGCGCGGCTA
976	GATGCCCTTTTGGTCCCCATGCCA	TGGCATGGGGACCAAAGGGCATC
977	TGAGCTGCCTTGCCACGATGCCTC	GAGGCATCGTGGCAAGGCAGCTCA
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	982	GCCGCCTCCGACTGGTTAACCCGA	TCGGGTAAACCAGTCGGAGGCGGC
	983	CGCACGGCTACTAACAGCGGATCA	TGATCCGCTGTTAGTAGCCGTGCG
	984	CCGGACCAATTCCAACGAGCATCG	CGATGCTCGTTGGAATTGGTCCGG
5	985	CATTGAGGTCCACC GTTCACATCC	GGATGTGAACGGTGGACCTCAATG
	986	AGGACGCAGCATGTCCAGCCGAG	CTCGGCTGGGACATGCTGCGTCCT
	987	TAATCGCGGGCCATACTACCAACG	CGTTGGTAGTATGGCCCGCGATTA
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	992	ACCTCGAGTCAGATTGTGCGCCTT	AAGGCGCACAACTGACTCGAGGT
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	997	ATCAGCGCAAGCTGGTCTGAAACA	TGTTTCAGACCAGCTTGCGCTGAT
	998	CCCTGGCCAGAACGAGAGGCCATG	CATGGCCTCTCGTTCTGGCCAGGG
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	1002	CGTAAATATCTGCGGCGGTGTGAA	TTACACCGCCGCAGATATTTACG
	1003	GGAAACACGTGTTCTGTCTGTTGGC	GCCAACAGACGAACACGTGTTTCC
	1004	CGATGTTAGGATTCGGATAGGCCA	TGGCCTATCCGAATCCTAACATCG
25	1005	ATCGGACAAGGACAAGTGGATGGT	ACCATCCACTTGTCTTGTCGGAT
	1006	GCCCGGAGGACAAAGTTTCGAGTTA	TAACTCGAACTTTGTCTCCGGGC
	1007	AAATCCGACAAATGGGCACATGGA	TCCATGTGCCCATTTGTCCGATTT
	1008	CAGTTAGGGGATGCGGATGAGTGA	TCACTCATCCGCATCCCCTAACTG
	1009	CGGCAGGTGGAGATTCCGACATTG	CAATGTGCGAATCTCCACCTGCCG
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	1011	GCACCGTATTAGCAGTAGGCACGC	GCGTGCCCTACTGCTAATACGGTGC
	1012	ACGCATTACAGGTGTGCGAAGGGA	TCCCTTCGCACACCTGTAATGCGT
	1013	CGTGACTGCACGTGTTCCACAGGG	CCCTGTGGAACACGTGCAGTCACG
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	1016	ATGAGGGCAAGGAATGGGTCATGC	GCATGACCCATTCTTGCCCTCAT
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	1018	TATCTTGCGCAACGCCTCCATTTA	TAAATGGAGGCGTTGCGCAAGATA
	1019	GGTTACACCTACGGAATCCAGCGG	CCGCTGGATTCCGTAGGTGTAACC
40	1020	ACACCGAGTTGGTCCGGTCAATAG	CTATTGACCGGACCAACTCGGTGT
	1021	TCCCAGATTAAACGCTAGCCACCG	CGGTGGCTAGCGTTTAACTGGGA



	1022	TTGGTGAAACTGGCCCGTCGGAAG	CTTCCGACGGGCCAGTTTCACCAA
	1023	CCAGGGGAGTTGACAATGAGGCTG	CAGCCTCATTGTCAACTCCCTGG
	1024	TCTGCGTTATTGGACCGTTTGTCTG	CGACAAACGGTCCAATAACGCAGA
5	1025	TATGGGATGCTAAACCGGCGTACA	TGTACGCCGGTTTAGCATCCCATA
	1026	CACAGACGTCTGTCTGGGCTTGTGT	ACACAAGCCCGACAGACGTCTGTG
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	1028	CGACGGATAATGCAGGCCTCATGA	TCATGAGGCCTGCATTATCCGTCTG
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	1036	CCGCTAAGCACCGAAGGCTCACAA	TTGTGAGCCTTCGGTGCTTAGCGG
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	1040	CGGGAAATGTCTTTAGCCGTGCAA	TTCGACGGCTAAAGACATTTCCCG
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	1042	GGCCTGTTTCTGTCCAAGTGGGCT	AGCCCAGTTGGACAGAAACAGGCC
	1043	ATTTCACTCGCTGATCGCTTCCG	CGGAAGCGATCAGCGAGGTGAAAT
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	1045	AGTTGTCTCATCCTGTCCGGGACC	GGTCCCGGACAGGATGAGACAAC
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	1048	ATGCGATCCATGACAAGGGTTGCT	AGCAACCCTTGTCATGGATCGCAT
	1049	CCCGTGGAGATGATGTGCGGCTTA	TAAGCCGCACATCATCTCCACGGG
	1050	CCCAATAGACGCCACAGCCAGTGA	TCACTGGCTGTGGCGTCTATTGGG
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	1053	CTGTGCGCGCTGCTCTCCGAATTT	AAATTCCGAGAGCAGCGCCGACAG
	1054	CTCGCCGGAGTGTTGTAAGCATTG	CAATGCTTACAACACTCCGGCGAG
	1055	AGCAATCATGAGAGGTGGCCGGTG	CACCGGCCACCTCTCATGATTGCT
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	1057	CCGCCCGTGTTGGCATGTCTTTTG	CAAAGACATGCCAACACGGGCGG
	1058	ATCGGAAGTGCTGACTGACACACG	CGTGTGTCAGTCAGCACTTCCGAT
	1059	CCTCAGACCCTATCTGGGTTGACG	CGTCAACCCAGATAGGGTCTGAGG
	1060	CTGTGTGGTCTGGTCCGGCTGTTT	GAACAGCCGGACCAGACCACACAG
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	1062	ACAGGCACGTAAGTGCTCAATCGG	CCGATTGAGCACTTACGTGCCCTGT

	1063	AGCAAGATAGCGGGAGTGCCCTA	TAGGGGCACTCCCGCTATCTTGCT
	1064	GGTTTACGCCATGACATCCCGTCA	TGACGGGATGTCATGGCGTAAACC
	1065	GTGCAGGCCTTTGTGTGTAATCG	CGATTCACACACAAAGGCCTGCAC
	1066	CTTCGAGGGTAGGGCTTCGAAACG	CGTTTCGAAGCCCTACCCTCGAAG
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	1068	ACATAAATCTCGCCCGCTGCACTC	GAGTGCAGCGGGCGAGATTTATGT
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	1073	CCTAAGTCGGTTTGCAGCTGCTCT	AGAGCAGCTGCAAACCGACTTAGG
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	1078	TGCTCAAGCTACGCGTCACTTCCC	GGGAAGTGACGCGTAGCTTGAGCA
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	1084	GAGGAGGCCAATAGAGCAGCGCGC	GCGCGCTGCTCTATTGGCCTCCTC
	1085	AGTAATCTTGCGGCACACAAGCGG	CCGCTTGTGTGCCGCAAGATTACT
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	1096	TTACCGGAATATGCACTTGCCCGC	GCGGCCAAGTGCAATTTCCGGTAA
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5	1107	CTTATCCCATGTGCCGGTCTGACT	AGTCAGACCGGCACATGGGATAAG
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10	1112	AGAATATGGGCAGCAGCAGCACTC	GAGTGCTGCTGCTGCCCATATTCT
	1113	CTGCAGTCGCACGCAGTAGACCCG	CGGGTCTACTGCGTGCGACTGCAG
	1114	ATGTCCCTGACCGGAATCTTTCCA	TGGAAAGATTCCGGTCAGGGACAT
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	1139	GAGAACCACAGGTGGTCCACCCTA	TAGGGTGGACCACCTGTGGTTCTC
	1140	CCTCGCTAGAGAAATCCACGGGAT	ATCCCGTGGATTTCTCTAGCGAGG
	1141	TAACATCGGTGCAAACCGTGCGC	GCGCCACGGTTTGACCGATGTTA
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	1143	AAAAGCGCTGCTCTAACACCGCCG	CGGCGGTGTTAGAGCAGCGCTTTT
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	1225	AGTCCGCGCGAAATACGAACAGTA	TACTGTTCGTATTTGCGCGGACT
	1226	ATGTTGCACGCGCACTGTATCACA	TGTGATACAGTGC GCGTGCAACAT

	1227	ATCGCCTAACTACCCGCGGCGTGC	GCACGCCGCGGGTAGTTAGGCGAT
	1228	TGGCCAGGGAACACAAGCTCGGTA	TACCGAGCTTGTGTTCCCTGGCCA
	1229	AAACATGGGTGCGCTCTGAGATCA	TGATCTCAGACGCGACCCATGTTT
5	1230	GCGAGAGCTGCGATTCCCTTTTAG	CTAAAAGGGAATCGCAGCTCTCGC
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	1232	AATGGGGCACAGTCTCGTTGACA	TGTCAAGCGAGACTGTGCCCCATT
	1233	TGTCTCGGGCCTTCAGGACACACT	AGTGTGTCTGAAGGCCCGAGACA
	1234	TCCACCTTCATTAAGTGGTTTCGGC	GCCGAACCACTTAATGAAGGTGGA
	1235	GCTTCGGAATCATCCACCTGTCAT	ATGACAGGTGGATGATTCCGAAGC
10	1236	GAGCCGATGGGCTATCGTCGTCGG	CCGACGACGATAGCCCATCGGCTC
	1237	CACGAATTACGCACGCACAGAGGA	TCCTCTGTGCGTGCGTAATTCGTG
	1238	GCTGTGACGCTCCCCTCAACTAGG	CCTAGTTGAGGGGAGCGTCACAGC
	1239	CGCTCTGAAAACGCGGGCTACGTT	AACGTAGCCCGCGTTTTTCAGAGCG
	1240	GAGTGCTGGACACCGTAGCCAGGA	TCCTGGCTACGGTGTCCAGCACTC
15	1241	CCAACCCAGTGTAGGCGCAAATG	CATTTGCGCCTACACTGGGGTTGG
	1242	GAAGTAGGGGATGTTGGCCGGCGG	CCGCCGGCCAACATCCCCTACTTC
	1243	CAACGTGGGCACCTGTTTTAGCAG	CTGCTAAAACAGGTGCCACGTTG
	1244	CTAGCTGCGATCCGAACCTCTACG	CGTAGAGGTTTCGGATCGCAGCTAG
	1245	CATTGAACCATCAGCCAAGCTGCG	CGCAGCTTGGCTGATGGTTCAATG
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	1247	CTGGCCGTCCATGAGTTGGTCCAG	CTGGACCAACTCATGGACGGCCAG
	1248	CATGCTGAAACACGGGATTGCCAT	ATGGCAATCCCGTGTTTCAGCATG
	1249	CGATATGTAAGACAGCCGTCGCAA	TTGCGACGGCTGTCTTACATATCG
	1250	AGCGTAACCTACTGGGAAGGCACC	GGTGCCTTCCCAGTAGGTTACGCT
25	1251	GTTCTGAACCCCGCGATGTTAAATG	CATTTAACATCGCGGGGTTTCAAC
	1252	GTTGTTAGGAGGCTCGAGGCTGCT	AGCAGCCTCGAGCCTCCTAACAAC
	1253	ACTGGTGCTACGCGGGATATTTGA	TCAAATATCCCGCGTAGCACCAGT
	1254	CTGGGAGCTATCCTCAGCCGAATC	GATTCGGCTGAGGATAGCTCCCAG
	1255	GAACTCGCCGCTGCCGAAGGGTAG	CTACCCTTCGGCAGCGGCGAGTTC
30	1256	TTGATCGAGGAGCAAGGAGAGTC	GACTCTCCTTGCTCCTCGATCGAA
	1257	GGGGAAAATTGAGGCCTTAGCCAT	ATGGCTAAGGCCTCAATTTTCCCC
	1258	CTAAGGTCAAAGCGCTGTCGCCAG	CTGGCGACAGCGCTTTGACCTTAG
	1259	CCGTAGCGGTGCTCGACCAGGTTT	GAACCTGGTCGAGCACCGCTACGG
	1260	TGGGGACGAATCCGAATGTAGTGA	TCACTACATTTCGGATTTCGCCCCA
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	1262	CTTTGCGCGGTGGTCAATAAAAAG	CTTTTTATTGACCACCGCGCAAAG
	1263	CTCGGGGATGCCCTCTTGGCATT	TAATGCCAAGAGGGCATCCCCGAG
	1264	CGAAACGTGGTGCAGAAACCTGAA	TTCAGGTTTCTGCACCACGTTTCG
	1265	GGAGTTCACGAGTCGAGCAGTCGC	GCGACTGCTCGACTCGTGAAGTCC
40	1266	AGCCGTTTTCAAAGATCTCGACGA	TCGTGAGATCTTTGAAAACGGCT
	1267	TGGCTGGACATTGTCTGCAATGCA	TGCATTGCAGACAATGTCCAGCCA

	1268	ATCGGCTGCCTCAGTCCCTAATTT	AAATTAGGGACTGAGGCAGCCGAT
	1269	CCAGCATGGAGTTAAGTGAGCGCG	CGCGCTCACTTAACTCCATGCTGG
	1270	TTCATATTTACGAATGCCGGGTGC	GCACCCGGCATTTCGTAAATATGAA
	1271	CGAAATCGCACAGGAATTCGCGTC	GACGCGAATTCCTGTGCGATTTCG
5	1272	GGCAATTTTCGGGACACTCGTTTCA	TGAAACGAGTGTCCCGAAATTGCC
	1273	TTTGTGATTGGGGGTATAACCCGA	TCGGGTTATAACCCCAATCACAAA
	1274	CCCAGCTAATCCAGCTTGGGCTGT	ACAGCCCAAGCTGGATTAGCTGGG
	1275	AAAATCGTTTGGCTGTAACGTCGC	GCGACGTTACAGCCAAACGATTTT
	1276	AGGAGATTCATCGACTTCCGGGAA	TTCCCGGAAGTCGATGAATCTCCT
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	1278	GCGCAACAAGTAGCCTACCGAGGC	GCCTCGGTAGGCTACTTGTGCGC
	1279	TAGCAGGCTGATGCCGTCTACACA	TGTGTAGACGGCATCAGCCTGCTA
	1280	GCAAGCGGCGATCGTACAATTGT	ACAAGTTGTACGATCGCCGCTTGC
	1281	GCACCTCTGGTAAGCCTGAAAGGG	CCCTTTCAGGCTTACCAGAGGTGC
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	1283	GGATTAACCGGAACTGCCCTTCTG	CAGAAGGGCAGTTCCGGTTAATCC
	1284	GATATTGGGTCCGGCGCGCATTAC	GTAATGCGCGCCGGACCCAATATC
	1285	GGCCTTTAATCTCCGGTCGCAATG	CATTGCGACCGGAGATTAAAGGCC
	1286	AACCTTAGTGCGGCTAGGTGGGGT	ACCCACCTAGCCGCACTAAGGTT
20	1287	CACGCTGACGCCAGTGTGGTGAGG	CCTCACCACACTGGCGTCAGCGTG
	1288	GGTTCCCTTGACCCACCGAATTGA	TCAATTCGGTGGGTCAAGGGAACC
	1289	TTCTGACAACATCGACCCTGGCTC	GAGCCAGGGTCGATGTTGTCAGAA
	1290	GCGAGCGAAGATAATCCCCAACT	AGTTTGGGGATTATCTTCGCTCGC
	1291	GTA CTCTGTGCAACGGTCCCAGT	ACTCGGGACCGTTGCACAGAGTAC
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	1293	AAGGGAATTTAGCGCGCGTGA CTT	AAGTCACGCGCGCTAAATTCCCTT
	1294	TGACGTACGCGTTTTAAGTGGGGA	TCCCCACTTAAACGCGTACGTCA
	1295	CTTAGAGGGACGAGGCCATGAATG	CATTCATGGCCTCGTCCCTCTAAG
	1296	GGACGACTCCGCAAAAAAGGTCGT	ACGACCTTTTTTGCGGAGTCGTCC
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	1298	GCACTGGTCTACCAAGCTTGTCCC	GGGACAAGCTTGGTAGACCAGTGC
	1299	ACTTGTGCGAAACGAGACCGAGCA	TGCTCGGTCTCGTTTCCGACAAGT
	1300	TCAGGAAAGGCCTAAAGGCGAAAG	CTTTCGCCTTTAGGCCTTTCCTGA
	1301	GGAATGTAGTCAAGGAGGACGGGG	CCCCGTCCTCCTTGACTACATTCC
35	1302	GCACGTGGTAAATGAATTGGCGAG	CTCGCCAATTCATTTACCACGTGC
	1303	GATCATCAGGGGTATGCGTCGCG	CGCGACGCATAACCCCTGATGATC
	1304	CTCACTCATTCTGATTGCCCGCGG	CCGCGGGCAATCAGAATGAGTGAG
	1305	GGGGTGATCTCTCGAACGTCACCC	GGGTGACGTTGAGAGATCACCCC
	1306	AAGGTTGCTGCTAGCGTACCTCGA	TCGAGGTACGCTAGCAGCAACCTT
40	1307	TATAGATCGCCCAACAGGCAGGAG	CTCCTGCCTGTTGGGCGATCTATA
	1308	GTTTGGACCTGTTGGGAGTGGGCA	TGCCCACTCCCAACAGGTCCAAAC

1309	ATTGGGGAAAACCCGGTCTCAAGG	CCTTGAGACCGGGTTTTCCCAAT
1310	TCGACGATAAAGTGCTCACGGGAC	GTCCCGTGAGCACTTTATCGTCGA
1311	CGATAGAATTCAATGCAGGGCGGA	TCCGCCCTGCATTGAATTCTATCG
1312	CGGTTTCGCTACGGCGGGCTGGTTTC	GAAACCAGCCGCCGTAGCGAACCG
1313	CCAGGTTTCGGTTAGTCGCGCTAG	CTAGCGCGACTAACCGAAACCTGG
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1315	TCGCGTTAAATGGACCAAGGGGCC	GGCCCCCTGGTCCATTTAACGCGA
1316	CCAGAAAGAAAATGGCGCCCGGAT	ATCCGGGCGCCATTTTCTTTCTGG
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1326	ACTTGCAACTTCGGCCGTTTGACT	AGTCAAACGGCCGAAGTTGCAAGT
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1331	CACAGAACAGGGTGTTTCCCGCTA	TAGCGGGAAACACCCTGTTCTGTG
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1345	GGAGGCATGCCCTCCGAGAGCAAC	GTTGCTCTCGGAAGGCATGCCTCC
1346	CACCGATCCTCAACGCAATTGCTA	TAGCAATTGCGTTGAGGATCGGTG
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1348	CTGTTCCAGGCGTAACCAGCGGGC	GCCCGCTGGTTACGCTGGAACAG
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	1350	GGAGTGACCAGCACAAAGCATCGAG	CTCGATGCTTGTGCTGGTCACTCC
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	1352	GTAGGGTCAAGCACGATTGAAGCC	GGCTTCAATCGTGCTTGACCCTAC
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	1356	GCGGACCTGGGTAAATTGACGCGC	GCGCGTCAATTAACCCAGGTCCGC
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	1370	TTTAGCCGCTGCGACTGTAGGAAA	TTTCCTACAGTCGCAGCGGCTAAA
	1371	ACTGTGTCGCAATCAACCCGCAAA	TTTGCGGGTTGATTGCGACACAGT
	1372	TGCAGCCAATGCGGAACTTAGAGG	CCTCTAAGTTCCGCATTGGCTGCA
	1373	CCCCTATCCCGGTCTTGACGTTT	GAAGTGAAGACCGGGATAGCGGG
25	1374	GAGGGCGCAACATATGCAGTGCTG	CAGCACTGCATATGTTGCGCCCTC
	1375	CGTACGGACATCGATGACGCAACG	CGTTGCGTCATCGATGTCCGTACG
	1376	AGTCTCCCGAGAAACGCATAAGGC	GCCTTATGCGTTTCTCGGGAGACT
	1377	AGGAAGTGGATGAACGCGGCTGCA	TGCAGCCGCGTTCATCCACTTCCT
	1378	GGGTTGCTCACCTCGTCATCAGG	CCTGATGACGAGGGTGAGCAACCC
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	1381	TCAATAGCACCTAGCATGCTCCCG	CGGGAGCATGCTAGGTGCTATTGA
	1382	TGATTCTGCGCTTTTCACAGGTCG	CGACCTGTGAAAGCGCAGGAATCA
	1383	GTATGTGCGGGATGGAATCACGC	GCGTGATTTCCATCCCGCACATAC
35	1384	TACGGCAACTGTGATACGAGGGC	GCCCTCGTATCGACAGTTGCCGTA
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	1386	ATAAGCGCGCCACAGGTATGTACC	GGTACATACCTGTGGCGCGCTTAT
	1387	GAAAGTCGCCAACAGACTCGAGCA	TGCTCGAGTCTGTTGGCGACTTTC
	1388	CGCTAATGCCTCATAGGCGTGTGC	GCACACGCCCTATGAGGCATTAGCG
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	1390	GACGCTGCTGATGGCTTTATCGAT	ATCGATAAAGCCATCAGCAGCGTC

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1393	GGCCTGAAGGTGAATGGTTACGTG	CACGTAACCATTCACCTTCAGGCC
1394	AGCCTCCAAAGCCGGTAGAGTTCC	GGAACCTACCGGCTTTGGAGGCT
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1396	GCCTGAGTCCGGGTCGGGAAAGAA	TTCTTTCCCGACCCGGACTCAGGC
1397	GGCACTATACCGGTTCTGGACGCG	CGCGTCCAGAACCAGGTATAGTGCC
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1427	GGTCGGAAGTATCTGTGCGATCC	GGATCGCACAGATCAGTTCCGACC
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	1432	GCGACGAAGAGATCCAGCAAGCTC	GAGCTTGCTGGATCTCTTCGTCGC
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	1447	CAGCAGCGTGCCCATCTCGACTTA	TAAGTCGAGATGGGCACGCTGCTG
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	1465	CAGCTACTAGGGCGCGATGTACCC	GGGTACATCGCGCCCTAGTAGCTG
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	1467	CGACCGAGTGTTACGACATGGTGC	GCACCATGTCGTAACACTCGGTG
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	1469	ATGCTAGCGCGCCTGTCAACGTAC	GTACGTTGACAGGCGCGCTAGCAT
	1470	AGACTCACTGCCGCTGATCAAAT	ATTTGATCAGCCGGCAGTGAGTCT
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1502	TACGTCCTGTGCTGTTGACACCGG	CCGGTGTCAACAGCACAGGACGTA
1503	GTTTCGGGTCAATGTTTCGGGGAGA	TCTCCCCGAAACATTGACCCGAAC
1504	CCCTGTTGTGAAGGGGTTTTGTGA	TCACAAAACCCCTTCACAACAGGG
1505	GGCAGATTGGTGAACCCAGATAA	TTATCTGGGGTTACCAATCTGCC
1506	CCCTCGGTGTGTTCAAGCCAAATC	GATTTGGCTTGAACACACCGAGGG
1507	CCCGCGAACATTTGAACAGCTTAA	TTAAGCTGTTCAAATGTTGCGGGG
1508	CCGTGTCAGTTGCTCCCTGGCACG	CGTGCCAGGGAGCAACTGACACGG
1509	TCCGTCTCAGCCGCTCCCTATCC	GGATAGGGAGGCGGCTGAGACGGA
1510	ATAGCTGGGTACACACAGGCGGTC	GACCGCTGTGGTGACCCAGCTAT
1511	ATAGGCAAGCGGTGTAGCACAGCG	CGCTGTGCTACACCGCTTGCTTAT
1512	TTAGAAGCCGGTCTGGATTTGCGT	ACGCAAATCCAGACCGGCTTCTAA
1513	TGCCGACCTTTACCAGGATCCTCG	CGAGGATCCTGGTAAAGGTGCGCA

	1514	GCCCACACTATAACCAAGCTGGCA	TGCCAGCTTGGTTATAGTGTGGGC
	1515	TTGCGCCACTAGTACGGATCTCAA	TTGAGATCCGTACTAGTGGCGCAA
	1516	CTTGCAGTTTATGCTGACCCGTCC	GGACGGGTCAGCATAAACTGCAAG
	1517	TGCCTCCAAATTACTTACCGCCGT	ACGGCGGTAAGTAATTTGGAGGCA
5	1518	CCCGTATGCGGAAGCTATGGGCTA	TAGCCCATAGCTTCCGCATACGGG
	1519	TCGTTCAACCCACACTTCAGTTG	CAACTGAAGTGTGGGGTTGAACGA
	1520	CAATGTGGGGGACATTTCAAGGTT	AACCTTGAAATGTCCCCACATTG
	1521	TAGCGTCGCACAAATGGCTGACCG	CGGTCAGCCATTTGTGCGACGCTA
	1522	GGTGGCTTCGTGACAATATCGGCC	GGCCGATATTGTCACGAAGCCACC
10	1523	CAGCGGCGTCCGAAATTGGCTCTC	GAGAGCCAATTTTCGGACGCCGCTG
	1524	GGCTTGCTCTCGTTTTTGATTGCA	TGCAATCAAAAACGAGAGCAAGCC
	1525	ATGCGAGGAGGACACGACCGTTCC	GGAACGGTCGTGTCTCTCTCGCAT
	1526	CCTGTTCACTACGACCCACGGGAA	TTCCCGTGGGTCGTAGTGAACAGG
	1527	GTGCCACGGAGTGCGACTGTTGCT	AGCAACAGTCGCACTCCGTGGCAC
15	1528	ACACATCCAAGTCTGACGATGGCC	GGCCATCGTCAGACTTGGATGTGT
	1529	CAGCCCGAAAGGAAAGCCTCCGTG	CACGGAGGCTTTCCTTTCCGGGCTG
	1530	AACTGAATGTAGGTGGGCCCTGT	ACAGGGGCCACCTACATTCACTT
	1531	ATTTTCGACGATAAGCTGGCCGGT	ACCGGCCAGCTTATCGTCGAAAAT
	1532	TGAGGGAGAACCCGAAATCTGCTT	AAGCAGATTTCCGGTTCTCCCTCA
20	1533	GGCGACTACATCCCAATTGCTTG	CAAGCAATTGGGGATGTAGTCGCC
	1534	GCAGACGCGGCCTTCCATACTTTT	AAAAGTATGGAAGGCCGCGTCTGC
	1535	ACAACCACATGACGTGTAGCTGCA	TGCAGCTACACGTCATGTGGTTGT
	1536	CTGCTGGGCGCGCAAAGCTTGTTG	CAACAAGCTTTGCGCGCCAGCAG
	1537	AAGCCTTCTTTGGCTTGCTCCGCT	AGCGGAGCAAGCCAAAGAAGGCTT
25	1538	TACCTGCTGCCTGGAGCAAGGCAT	ATGCCTTGCTCCAGGCAGCAGGTA
	1539	GACGCCGCAGCCATGAGTGAGTGT	ACACTCACTCATGGCTGCGGCGTC
	1540	AGTTGGCCGCTTATTTTGTCTACC	GGTGAGCAAAATAAGCGGCCAACT
	1541	CCAGGCGCCTTCGACAGATCCTCA	TGAGGATCTGTGCAAGGCGCCTGG
	1542	GTGTCCCCTCCAGCTAGCCAGTTT	AAACTGGCTAGCTGGAGGGGACAC
30	1543	GACAACAAGCCAAGGTGACACGTC	GACGTGTACCTTGGCTTGTGTGTC
	1544	CTACACCGCTCGTGACTCGGCAAA	TTTGCCGAGTCACGAGCGGTGTAG
	1545	TGGTGCCATCAAAGCACGTTGTAC	GTACAACGTGCTTTGATGGCACCA
	1546	ACAATGCGTGTTGCGAAACGCATA	TATGCGTTTCGCAACACGCATTGT
	1547	TTGTCCAGCCATTGTATTTGCGC	GCGCAAAATACAATGGCTGGACAA
35	1548	ACGAGAGATAGCGGACTCCTCCGA	TCGGAGGAGTCCGCTATCTCTCGT
	1549	AGCTTTGTGCTCAGGCGAGCTCTT	AAGAGCTCGCCTGACGACAAAGCT
	1550	GACAGTCGGCGTGACGTTTGTGT	ACAACAACTGCACGCCGACTGTC
	1551	AGCTAGCGACGGCCAACTCACGTA	TACGTGAGTTGGCCGTCGCTAGCT
	1552	CTCCTGTTCCGGGGCCGTTACTGGT	ACCAGTAACGGCCCCGAACAGGAG
40	1553	ACTGACCGACGCAGTGCCACATAG	CTATGTGGCACTGCGTCGGTCAGT
	1554	AGGTAGGGTCTGTTTGACTCGCA	TGCGAGTCAAACCAGACCCTACCT

5	1555	CCTCCATTTTAGCGCGTTGCCAAT	ATTGGCAACGCGCTAAAATGGAGG
	1556	TTCTTAGGATCCGCGCACTCTTGG	CCAAGAGTGCGCGGATCCTAAGAA
	1557	GTCGAAGGTGTCTACCGTGCGCAG	CTGCGCACGGTAGACACCTTCGAC
	1558	GTCACCTCGGCGGCCCAATCACTCG	CGAGTGATTGGGCCGCCGAGTGAC
	1559	TCTCGGTCACCCGTCTTGACCCTT	AAGGGTCAAGACGGGTGACCGAGA
	1560	GCCCTCGACGAACTCATCCTGAAC	GTTCAGGATGAGTTCGTGAGGGC
	1561	TCCGGCGTACTCTGACACGGCGAT	ATCGCCGTGTCAGAGTACGCCGGA
	1562	AGCCAAATGCTTTTCGTGGTTCGGA	TCCGAACCACGAAAGCATTGCGCT
	1563	ACTCCACGCCGCATGTTGCTGTGA	TCACAGCAACATGCGGCGTGAGT
10	1564	GCTTCGAGTCGGTGGCATCTGTAT	ATACAGATGCCACCGACTCGAAGC
	1565	GGTCTTGGGCCATCGACTTGCTGC	GCAGCAAGTCGATGGCCCAAGACC
	1566	GGTATCGGACTGCACTAAGGGCAA	TTGCCCTTAGTGCAGTCCGATACC
	1567	AGCCCATGCGTTCCGGATGATTTG	CAAATCATCCGGAACGCATGGGCT
	1568	GCCAGGGTTAAAAGTGATGGGCTC	GAGCCCATCACTTTTAACCCTGGC
15	1569	GACGACGTGCTGGCTACGAAGGGG	CCCCTTCGTAGCCAGCACGTCGTC
	1570	TCCTATTGACCGTGCATCGTGATC	GATCACGATGCACGGTCAATAGGA
	1571	ACCCGCCTCGACTCCACAATAAA	TTTAGTTGTGGAGTCGAGGCGGGT
	1572	GATGTGGATCACGACCTGCCAGTA	TACTGGCAGGTCGTGATCCACATC
	1573	GTGCCATTGCCACCCATAATGCGT	ACGCATTATGGGTGGCAATGGCAC
20	1574	TTAGCCTGTGCACCCAGTCAGGAG	CTCCTGACTGGGTGCACAGGCTAA
	1575	TCCGATGGGAGAGGCTGATCTCAC	GTGAGATCAGCCTCTCCCATCGGA
	1576	CACTACTGAAGTGGCCTGGCGCTG	CAGCGCCAGGCCACTTCAGTAGTG
	1577	TGCGGCCATAGCGATGTGATAGAT	ATCTATCACATCGCTATGGCCGCA
	1578	GATTGCGCTTAACGGAGATGCACG	CGTGATCTCCGTTAAGCGCAATC
25	1579	TCACGTTTGACAACGCCAAGCATT	AATGCTTGGCGTTGTCAAACGTGA
	1580	GCATTGTTTGCTAAAGGCGGCATT	AATGCCGCCTTTAGCAAACAATGC
	1581	AGTCGCTCTACGCGTGCAACGCTG	CAGCGTTGCACGCGTAGAGCGACT
	1582	TAGCTCCATGGAGGTCCGAAAGGG	CCCTTTCGGACCTCCATGGAGCTA
	1583	GACCGGTTGGACCTCACTGGCTTC	GAAGCCAGTGAGGTCCAACCGGTC
30	1584	AAGCCGGACAGTCAATGTGCGTAT	ATACGCACATTGACTGTCCGGCTT
	1585	TGCCTCGCTGAGTTCTTCACCGTG	CACGGTGAAGAACTCAGCGAGGCA
	1586	TCGTAGACCTTGCTTTTGGGCTCA	TGAGCCCAAAGCAAGGTCTACGA
	1587	ACCGCTATGCGCCCTACAAAGCAT	ATGCTTTGTAGGGCGCATAGCGGT
	1588	TAGCGTCACCGTAGCTTGGGGCAG	CTGCCCAAGCTACGGTGACGCTA
35	1589	CTCTCAGCAACTGATGGCACCGGA	TCCGGTGCCATCAGTTGCTGAGAG
	1590	AAAGGAAATGTGGTGCTGGTCGGC	GCCGACCAGCACCACATTTCTTT
	1591	CCGGCTTAGATGGAGAACAAGTGC	GCACTTGTTCTCCATCTAAGCCGG
	1592	AAGTAAATCGCCTCGCCCAAACCG	CGGTTTGGGCGAGGCGATTACTT
	1593	TGGGCTGTTACGCCTACCGGACGT	ACGTCCGGTAGGCTGAACAGCCCA
40	1594	GTTTCGGTTCAGCCATGGGCCTAC	GTAGGCCCATGGCTGAACCGAAAC
	1595	GGCCAACATTTCTAGGGGAGTGCC	GGCACTCCCCTAGAAATGTTGGCC

1596	TTCTTCGTTGGGATTGTCCTCACC	GGTGAGGACAATCCCAACGAAGAA
1597	TGCACATTGGGGTACGGATCTGAC	GTCAGATCCGTACCCCAATGTGCA
1598	GGCAGTTAGACGGCAAACCTGCAGG	CCTGCAGTTTGCCGTCTAACTGCC
1599	CGCGTCAGGCTATGAATGGCTCTT	AAGAGCCATTCATAGCCTGACGCG
1600	GCTGAATGCAAACCTCGGAGCCAT	ATGGCTCCGAGGTTTGCATTGAGC
1601	CGCTCTGGCGGATTCATTGTTTTT	GAAAACAATGAATCCGCCAGAGCG
1602	TTTTCAATCAACCCTCCGGACGTA	TACGTCCGGAGGGTTGATTGAAAA
1603	GTGGTGGAGTCTGAAGCACGACAG	CTGTCTGTCTTCAGACTCCACCAC
1604	AAACAGGTCCGGATGATGTCTGGA	TCCAGACATCATCCGGACCTGTTT
1605	GTACCGCGTGTACGCCACCGTTAG	CTAACGGTGGCGTACACGCGGTAC
1606	TCCAACCTACATTTGCGGAAGGAA	TTCCTTCCGCAAATGTAGGTTGGA
1607	GACGTACCGTCGTCCCGTGAGTTG	CAACTCACGGGACGACGGTACGTC
1608	GGCAATCCTACAACCGACGCTGAT	ATCAGCGTCGGTTGTAGGATTGCC
1609	GGCGGCTGCAGGGTCTACATCGAG	CTCGATGTAGACCCTGCAGCCGCC
1610	ATACTACGCTGCAGCTGCGCGGGC	GCCCGCGCAGCTGCAGCGTAGTAT
1611	GGATCGCAATCCCTCCGATGACGA	TCGTATCGGAGGGATTGCGATCC
1612	TGGCCTTGACGCGGAGCCGAATCT	AGATTGCGCTCCCGTGCAAGGCCA
1613	AGGTGCCGACGAAACGACGAATAT	ATATTGTCGTTTCGTGCGCACCT
1614	GCTGTTTCACCGTCGTGTTGTTG	CAACAACGACGACGGTGAAACAGC
1615	CGGTCCCAATGTTACAACCCAGAC	GTCTGGGTTGTAACATTGGGACCG
1616	GCAATTCCAGCCACTTTTGACCAA	TTGGTCAAAAGTGGCTGGAATTGC
1617	ACGGGCGAAAGCTCGGTACGGATA	TATCCGTACCGAGCTTTCGCCCGT
1618	CGACCCGACTTTTGCTTTCGAGTG	CACTCGAAAGCAAAAGTCGGGTCG
1619	AATTCAGTGTTTGCGTCATGGTCG	CGACCATGACGCAAACTGAATT
1620	CCTGTATGAGGTTCTGGGTCGGCT	AGCCGACCCAGAACCTCATACAGG
1621	TGGCATACTTGGTGCAAACGCCGT	ACGGCGTTTGACCAAGTATGCCA
1622	TCGCCAGTACAGAAACATGCGGGC	GCCCGCATGTTTCTGTACTGGCGA
1623	CCCGCTGTTGCTCTCATCGTGGAG	CTCCACGATGAGAGCAACAGCGGG
1624	GCCACAATCTGACCCTGGAATCA	TGATTCCCAGGGTCAGATTGTGGC
1625	GCTCAGTCTCGGAAGTTTCGGCTA	TAGCCGAAACTTCGAGACTGAGC
1626	CTTCACGGGCCAACGACGGTCGAG	CTCGACCGTCGTTGGCCCGTGAAG
1627	CGACAGTTCGGTCCGTCTTGAGGA	TCCTCAAGACGGACGGAACGTGTCG
1628	ACGGAGACGCAGTCGAAACGTCCC	GGGACGTTTCGACTGCGTCTCCGT
1629	CATGCATCCGATTAAGGGGATCAC	GTGATCCCCTTAATCGGATGCATG
1630	ATTGCGGGAGTCCCTAGCTTTCTG	CAGAAAGCTAGGGACTCCCGCAAT
1631	GTGTGGAAGATGCAATTGGAACGG	CCGTTCCAATTGCATCTTCCACAC
1632	ATACAACGGTAGGTGACAGGGGCG	CGCCCCTGTACCTACCGTTGTAT
1633	GCCGTGGGAGTAAGGTACAAAGG	CCTTTGTACCCTTACTCCCACGGC
1634	GCACGTAGGTGCGCTACTACTCGG	CCGAGTAGTAGCCGACCTACGTGC
1635	ACTGTGATCTCTTGGGCAAAGGGC	GCCCTTTGCCCAAGAGATCACAGT
1636	CATGCCTGAACAATCTCGCATCCC	GGGATGCGAGATTGTTTCAGGCATG

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1637	GAGCCTGGCTCCACAGCTGTGCTC	GAGCACAGCTGTGGAGCCAGGCTC
1638	CTTTCGATACCATCGTTGGCGATC	GATCGCCAACGATGGTATCGAAAG
1639	CCCGGAGGTGAGGCATTGAATATG	CATATTCAATGCCTCACCTCCGGG
1640	CTCATTCACTAAAAGCGGCTGGA	TCCAGCCGCTTTTAGCTGAATGAG
1641	GAAATGCCCTGGGGACTTTTTGCC	GGCAAAAAGTCCCCAGGGCATTTC
1642	TTTGCCTTCACAACAGACGCAGCA	TGCTGCGTCTGTTGTGAAGGCAAA
1643	AAATCCCAAGACGTCGGGGCGTAT	ATACGCCCCGACGTCTTGGGATT
1644	CAACGGGCGGTAGCTAAACCGTAA	TTACGGTTTAGCTACCGCCCGTTG
1645	GGCCAACGACAATGCGAAACCTTC	GAAGGTTTCGCATTGTCGTTGGCC
1646	GACATCACGCAAAATCTCAGCGCA	TGCGCTGAGATTTTGCCTGATGTC
1647	ACGTTCCGTCCACAACCGTATGTT	AACATACGGTTGTGGACGGAACGT
1648	GCTCATAGGTCTTCCGTAGCCCGT	ACGGGCTACGGAAGACCTATGAGC
1649	GAAACGAGTCTCTCGCGCCCTAGA	TCTAGGGCGCGAGAGACTCGTTTC
1650	CGGGACAGAAGCAAGTTACATCGG	CCGATGTAACCTGCTTCTGTCCCG
1651	TGACCGCTCGATACCAGGAGGGTG	CACCCTCCTGGTATCGAGCGGTCA
1652	CTGGCAATAAAGACCTTCCGACCA	TGGTCGGAAGGTCTTTATTGCCAG
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1654	GTTGGTTGTGGGAACACACCCGCT	AGCGGGTGTGTTCCCAACCAAC
1655	TGTGGGTTCGGAAACACAGGAAGT	ACTTCCTGTGTTCCGAACCCACA
1656	GGAAAAACGGCAATTAGCCGAGT	ACTCGGCTAATTGCCGTTTTTCC
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1659	AAACAGATCCATCTGCACGCCAGG	CCTGGCGTGCAGATGGATCTGTTT
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1661	TACTGTTGCGGCAAACCGTCACT	AGTGACGGTTTGCCGCAACAGTA
1662	GATCTCTCGTGGAGCACGTTTTCC	GGAAACGTGCTCCACGAGAGATC
1663	GGCATAGCAAACCTTGACCTCCAA	TTGGAGGTCAAGGTTTGCTATGCC
1664	ATCTGGGATTCGCGAGCCAATATC	GATATTGGCTCGCGAATCCAGAT
1665	CGATCAGGATATCATTTACGCCCG	CGGGCGTAAATGATATCCTGATCG
1666	ACGGTACCGAAACGGTCTCAGCGT	ACGCTGAGACCGTTTCGGTACCGT
1667	CTCCCATACCTGCGTTCTTACCGA	TCGGTAAGAACGCAGGTATGGGAG
1668	GCACGAGAACCTAATTGTGCACAA	TGTGCGACAATTAGGTTCTCGTGC
1669	GCCACACGATCAAGACAGCGCATG	CATGCGCTGTCTTGATCGTGTGGC
1670	CCCGTTAACTCACGAGCGGTCAAT	ATTGACCGCTCGTGAGTTAACGGG
1671	AGAGAAGGTCATTGCCTGTCGGTG	CACCGACAGGCAATGACCTTCTCT
1672	CGGGCCCTCTTAAAGTAGAGCAGG	CCTGCTCTACTTTAAGAGGGCCCG
1673	ACATCGCGTCCGAGGGAGTTAGCG	CGCTAACTCCCTCGGACGCGATGT
1674	AATGCCTAATCGAGCCAGCGGATC	GATCCGCTGGCTCGATTAGGCATT
1675	CTCGATCTTTTTAAACGGCGCTT	AAGCGCCGTTTAAAAAGATCGAG
1676	CGTTCCTGGAAGGCAGGGTCTCAC	GTGAGACCCTGCCTTCCAGGAACG
1677	CCTGTGCTTACTATCGGCGATCCA	TGGATCGCCGATAGTAAGCACAGG



	1678	GTTAGTCGCCCTATTGGCCTGGTT	AACCAGGCCAATAGGGCGACTAAC
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	1680	CGTGGTTTAAACATCGCGCTTCG	CGAAGCGCGATGTTTTAAACCACG
5	1681	TAAGACGCAGAAGATGGGGTCCAC	GTGGACCCCATCTTCTGCGTCTTA
	1682	CACCACAGCTTCTTTGTTGACCC	GGGTGGAACAAAGAAGCTGTGGTG
	1683	TCGGGTCCGTACCACCACTTTTGC	GCAAAAGTGGTGGTACGGACCCGA
	1684	CCAAGCCCCGAGTACCGAAGATTT	AAATCTTCGGTACTCGGGGCTTGG
	1685	TCCGTGATATGGTCGTGGCGCGGT	ACCGCGCCACGACCATATCACGGA
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	1687	AGGACTGCACTGTGCACGTCTGAT	ATCAGACGTGCACAGTGCAGTCCT
	1688	CCATCCTCATGTACAGCGCCGCTG	CAGCGGCGCTGTACATGAGGATGG
	1689	GTACCCGCGCCTTCCTCGACACAG	CTGTGTGAGGAAGGCGCGGGTAC
	1690	ACGGGTCCTGGTCGACTAAGGCTT	AAGCCTTAGTCGACCAGGACCCGT
15	1691	CGTATCGAAGGCGTGTACAACCGG	CCGGTTGTACACGCCTTCGATACG
	1692	TGCCCGCCCTTTATGCAACGCTCA	TGAGCGTTGCATAAAGGGCGGGCA
	1693	AAACTTACGAGACGGCGGCTGCCA	TGGCAGCCGCCGTCTCGTAAGTTT
	1694	AAGTCTGACAAACGGAACGGGTGT	ACACCCGTTCCGTTTGTCAGACTT
	1695	TAAGCGCAGACCAAAGTATGCGGC	GCCGCATACTTTGGTCTGCGCTTA
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	1697	TCGGAAGCATTTACGCGATCTCAG	CTGAGATCGCGTAAATGCTTCGGA
	1698	CACAGAAACGGTTGAACGAACGCC	GGCGTTTCGTTCAACCGTTTCTGTG
	1699	GCATGCTCAGATGGTCGTGCTCAC	GTGAGCACGACCATCTGAGCATGC
	1700	AAGGATTCTCGCTTCCGGCATGAT	ATCATGCCGGAAGCGAGAATCCTT
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	1702	ATTATTACGGGACCGAACCAACGG	CCGTTGGTTCGGTCCCGTAATAAT
	1703	GCGCGAGTGTCATGATGTTACGT	ACGTGAACATCATGACACTCGCGC
	1704	GACATTCGTGACTTGGTCGTCCGC	GCGGACGACCAAGTCACGAATGTC
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30	1706	GAGTTGTGCGGAGTCATCGGAGTC	GACTCCGATGACTCCGCACAACCTC
	1707	GCCTTTACAGATTTGGCGGGCTAT	ATAGCCCGCCAAATCTGTAAAGGC
	1708	ATGGCGTTTGCGAAGTCGATACAG	CTGTATCGACTTCGCAAACGCCAT
	1709	TGCATCGGCCTCAATCAGAGAACT	AGTTCTCTGATTGAGGCCGATGCA
	1710	ACAATCATGGCAATCTGGCAAATG	CATTTGCCAGATTGCCATGATTGT
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	1712	AGGGCAGGGGACGGACAGTAAGTC	GACTTACTGTCCGTCCCCTGCCCT
	1713	GCATAGGGCGAATCTAGTACGGGC	GCCCGTACTAGATTGCCCTATGC
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	1715	TGGCCGCTTCCACTAATATTGGAC	GTCCAATATTAGTGGAAGCGGCCA
40	1716	CCGGCGGACGGCTCTTGTCAATGA	TCATTGACAAGAGCCGTCCGCCGG
	1717	CGAGCAACCCAAAAGGAAGCAGTA	TACTGCTTCCTTTTGGGTGCTCG
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	1719	AGTACCGCTACAACGCTGGTTCGC	GCGAACCAGCGTTGTAGCGGTACT
	1720	GGGCAGGCCAGGTCCACCTGAGAA	TTCTCAGGTGGACCTGGCCTGCCC
	1721	CCACTTCTGTGACCGAACCCTGCT	AGCACGGTTCGGTCACAGAAAGTGG
	1722	CCTGGTACCAGGCAGCAGTTGATT	AATCAACTGCTGCCTGGTACCAGG
5	1723	TTAGGGTACCGTCGAGAGACGCCA	TGGCGTCTCTCGACGGTACCCTAA
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	1725	TGCTTCGACCGATGAACTCGAAG	CTTCGAGTTTCATCGGTCTGAAGCA
	1726	TGCCACCCATACTATGCCAGTGG	CCACTGGGCATAGTATGGGTGGCA
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	1729	TATTGCGAATTCGAGTACGTGCCC	GGGCACGTAATCGAATTCGCAATA
	1730	CGAGAGGGGTTCCCAAGTGATCGA	TCGATCACTGGGGAACCCCTCTCG
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	1732	GTGCGTCATTGTGGGTCATCCCAA	TTGGGATGACCCACAATGACGCAC
15	1733	AGGGCTCCCAGCATACCAACGTTG	CAACGTTGGTATGCTGGGAGCCCT
	1734	AACTAGCCGCACCTTTGTGCAGAG	CTCTGCACAAAGGTGCGGCTAGTT
	1735	TTAGCCCAGCCCTTCAATGGGAAC	GTTCCCATTAAGGGCTGGGCTAA
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	1737	TCTTTGAGGCGCGGACCCGCATAT	ATATGCGGGTCCGCGCCTCAAAGA
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	1739	GAGATTCAATACAGGCCGCGGGTC	GACCCGCGGCCTGTATTGAATCTC
	1740	AGGGCGAAGGAAGGTTCCGTTTTT	AAAAACGGAACCTTCCTTCGCCCT
	1741	CTCGACCCCTGCCACTACTGGTTC	GAACCAGTAGTGGCAGGGGTCGAG
	1742	TGTTCCGCGGTCTACGCATTACTG	CAGTAATGCGTAGACCGCGGAACA
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	1744	AGATTGCGACAGCGACACGTGATT	AATCACGTGTGCTGTGCGCAATCT
	1745	GATACCGTTGGCATTCTCGGTA	TACCGAGAAATGCCAACGGTATC
	1746	GATTGGGAGGCATTACGCGACGGA	TCCGTGCTGAATGCCTCCCAATC
	1747	AGGAGGAAACGAGGGCGTAGGTTT	GAACCTACGCCCTCGTTTCCTCCT
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	1749	TTTAATGCGGAAAGGATGCACGCG	CGCGTGCATCCTTTCCGCATTAAA
	1750	TTATCGGCCGTTAAAATGGGATGG	CCATCCCATTTAACGGCCGATAA
	1751	CCTTGGATTCTGTCATCGCTAGCA	TGCTAGCGATGAACGAATCCAAGG
	1752	AAGTGAACGTGCAGTGGTCTTCGA	TCGAAGACCACTGCACGTTCACTT
35	1753	TCCTTACCCCTCGTTCAAACGCCT	AGGCGTTTGAACGAGGGGTAAGGA
	1754	ATTCTGAACCATGCATGGCCTGT	ACAGGCCATGCATGGTTCAGGAAT
	1755	AGCGAGACGCTCGATCACGAACCTA	TAGTTCGTGATCGAGCGTCTCGCT
	1756	GCTGGTCTGGCTCGCTGTTTAGAA	TTCTAAACAGCGAGCCAGACCAGC
	1757	CGTGCGCGGCATAAAGATAGGTCT	AGACCTATCTTTATGCCGCGCACG
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	1760	TCCAGGGTCGGAGTACATGGCGGG	CCCGCCATGTACTCCGACCCTGGA
	1761	ATATGCCGTCGGATCGTACACGCA	TGCGTGACGATCCGACGGCATAT
	1762	TGCTGGCGTCAACACTTCCCGATT	AATCGGGAAGTGTTGACGCCAGCA
	1763	CAGGGCGGTGCGGTGAACTAGCCA	TGGCTAGTTCACCGCACC GCCCTG
5	1764	CATGGACTGCCGTACATCAGCTGG	CCAGCTGATGTACGGCAGTCCATG
	1765	CCGGCCATACGCTGGCAAGATTAC	GTAATCTTGCCAGCGTATGGCCGG
	1766	AGCGGACACCTGTACTCTCCTCCA	TGGAGGAGAGTACAGGTGTCCGCT
	1767	GGAGCCACACCAGTCGAAGATGGT	ACCATCTTCGACTGGTGTGGCTCC
	1768	CGCCACCGGAAATTGAAAAGACTG	CAGTCTTTTCAATTTCCGGTGGCG
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	1770	TTGAAGCGGTGAAGAGCCTGTCCT	AGGACAGGCTCTTCACCGCTTCAA
	1771	CGAACCAAGCTGCATTGTCACTGG	CCACTGACAATGCAGCTTGGTTCCG
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	1773	GCTGGGTATAGTTGCCTGGCAATG	CATTGCCAGGCAACTATACCCAGC
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	1776	TGGCGTTCAGTCAACGCTGGTTA	TAACCAGCGTTGCACTGAACGCCA
	1777	CAAACTGACGGGTATGGGAGCGC	GCGCTCCCATACCCGTCAGTTTTG
	1778	AGGTGTCGCTGGAACCCGACTTGT	ACAAGTCGGGTTCCAGCGACACCT
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	1780	TCGGGCTTCTCGCAATTCTGTCAG	CTGACAGAATTGCGAGAAGCCCGA
	1781	GCCAAAAGAATGCGCTGGGTAGGT	ACCTACCCAGCGCATTCTTTTGGC
	1782	TGGTGCCCGCACCGAGAGACTGTA	TACAGTCTCTCGGTGCGGGCACCA
	1783	CGAGGCCGTAAGTGGGGACTGCTCT	AGAGCAGTCCCCACTACGGCCTCG
25	1784	CGATCTGCGCATAGAGGGGACTTT	AAAGTCCCCTCTATGCGCAGATCG
	1785	TGTGCAATCGGCCCTTCTCAGAGCC	GGCTCTGAGAAGGCCGATTGCACA
	1786	GATCACCTGGACCGCTACCGTTTT	AAAACGGTAGCGGTCCAGGTGATC
	1787	ATGGGGAGTTAAGGACCCTGCACC	GGTGCAGGGTCCTTAACCTCCCAT
	1788	CATTGTGGACAGCCAATGGTGGCT	AGCCACCATTGGCTGTCCACAATG
30	1789	CCATCACCATGCCACGGTAAGATC	GATCTTACCGTGGCATGGTGATGG
	1790	GCACCCGTGTCGTTGGTTAGCAAG	CTTGCTAACCAACGACACGGGTGC
	1791	GGAGTGGGTTCCGCGAATTCAGTG	CAGTGAATTCGCGGAACCCACTCC
	1792	GGGGATTTCTTTTCGCAGGCTCGA	TCGAGCCTGCGAAAGGAAATCCCC
	1793	CATTGATCATGTGCACTTGACCA	TGGTGCAAGTGACATGATCAATG
35	1794	AGCAGCGCTGCGCTTGTTCGGAT	ATCCGAAACAAGCGCAGCGCTGCT
	1795	CGAGTAACGCGGTTGCTTTGCGAA	TTGCGAAAGCAACCGCGTTACTCG
	1796	TGGCCTGGAACATAGGTGGAATC	GAGTTCCACCTATGTTCCAGGCCA
	1797	CGCACACCAAGCGTTTATTGAGAA	TTCTCAATAAACGCTTGGTGTGCG
	1798	TCACCTTCACAGTGGGCATACAGC	GCTGTATGCCCACTGTGAAGGTGA
40	1799	CAAATATCCCTGAGCCCTCGAGCT	AGCTCGAGGGCTCAGGGATATTTG
	1800	GGGAGCTGGTGAGCAGATGTAACG	CGTTACATCTGCTCACCAGCTCCC

	1801	AGGATTGCTTTTGC GTTATGCGGA	TCCGCATAACGCAAAAGCAATCCT
	1802	ATCGTTTGGGCGCTACGCAATTGT	ACAATTGCGTAGCGCCCAAACGAT
	1803	CCGATTTGTCCCAAATGCAACGTT	AACGTTGCATTTGGGACAAATCGG
	1804	AAGGGTCAAGCTCATGGAGCGGAA	TTCCGCTCCATGAGCTTGACCCTT
5	1805	TCTGACGTCGTTCAAGGGCTCGCT	AGCGAGCCCTTGAACGACGTCAGA
	1806	CGCACCACTCCGAGGTATTTGTCT	AGACAAATACCTCGGAGTGGTGCG
	1807	AAGGGGTGAAAAAGGAGAAGCCGA	TCGGCTTCTCCTTTTTACCCCTT
	1808	AAACCACGCAAATGGCGATACCAT	ATGGTATCGCCATTTGCGTGGTTT
	1809	CAGAAGGGATGACGCCTTAAGTCG	CGACTTAAGGCGTCATCCCTTCTG
10	1810	CATGACGAGAGCGGACCTGAAGTG	CACTTCAGGTCCGCTCTCGTCATG
	1811	CTGGACATGTTTGTTCGCCACTG	CAGTGGCGAAACAAACATGTCCAG
	1812	AAGACCGACTCTCGTCGTTGCAC	GTGCAAACGACGAGAGTCGGTCTT
	1813	GCGCGATTACATACCGTTTCCGTA	TACGGAACGGTATGTAATCGCGC
	1814	CACTGACCGGACCCAAACCTAACAT	ATGTTAGGTTGGGTCCGGTCAGTG
15	1815	AGTGCAAGTCTAGACACGCCCGAG	CTCGGGCGTGTCTAGACTTGCACT
	1816	GGTTGGTGCGAGATCCTGGACTGT	ACAGTCCAGGATCTCGCACCAACC
	1817	GGTCGTCCCGAAACGTAACGAGG	CCTCGTTTACGTTTCGGGACGACC
	1818	GACTAGTACGATCACGGGGCGGGT	ACCCGCCCGGTGATCGTACTAGTC
	1819	CCGACCTGACCCTGTGTACAGGTT	AACCTGTACACAGGGTCAGTCCGG
20	1820	TGCTCACTGCCCACACTGTTATGG	CCATAACAGTGTGGGCAGTGAGCA
	1821	CGAGGAAACACATTTCTTCGGGCC	GGCCCGAAGAAATGTGTTTCCTCG
	1822	TGGCACCGGGTGGATTCTTGTCTA	TAGACAAGAATCCACCCGGTGCCA
	1823	GAGGCACGGTGATAGTGGTTGTGC	GCACAACCACTATCACCGTGCCTC
	1824	ATGCAGATGGATCTTTTTCGACGC	GCGTCGAAAAAGATCCATCTGCAT
25	1825	TGCGATAGCCAAAGAGTCGAGGAC	GTCCTCGACTCTTTGGCTATCGCA
	1826	ATGGCGTGTGACGGAAGTGCCTGG	CCAGGCAGTTGCTGACACGCCAT
	1827	CAATGCAGCTCGGAAGTCAGGTCG	CGACCTGACTTCCGAGCTGCATTG
	1828	AGGATCAGTGACATGTCCCCTCA	TGAGGGGACATGTGCACTGATCCT
	1829	CACATCTTGGCTGTACCCGAGAA	TTCTCGGGTGACAGCCAAGATGTG
30	1830	CGCATTATCACCTCAATGCCAGTG	CACTGGCATTGAGGTGATAATGCG
	1831	ACATCCGCAGACTCCCTATAGCCC	GGGCTATAGGGAGTCTGCGGATGT
	1832	GTGAACCCGAACGAGGGGAGTCTC	GAGACTCCCCTCGTTCGGGTTTAC
	1833	GCGTAGGGAAATTTGCCTCACGACT	AGTCGTGAGGCAAATTCCTACGC
	1834	TTTACGCGTCGCTCGGTTGTAGTG	CACTACAACCGAGCGACGCGTAAA
35	1835	GAGAGGCGTCTAGGCGGTTCTAGC	GCTAGAACCGCCTAGACGCCTCTC
	1836	GCATGCTGATAACGAATGCTTCCC	GGAAGCATTTCGTTATCAGCATGC
	1837	CTGAAGCTCGTGTGCGATGAGGGA	TCCCTCATCGCACACGAGCTTCAG
	1838	ACAACGGCATGAGGAGGCTTTTTT	GAAAAAGCCTCCTCATGCCGTTGT
	1839	TTTGGAGACGCCAGTACGCGTGGT	ACCACGCGTACTGGCGTCTCCAAA
40	1840	GCTATCATTTGGTGTAAGCCCGCC	GGCGGGCTTACACCAAATGATAGC
	1841	TCAACATCCAGGGCGGTGCTTGGT	ACCAAGCACCGCCCTGGATGTTGA

	1842	TTCGATGTAATCCCCAAGATGCC	GGCATCTTTGGGGATTACATCGAA
	1843	GGACCTTCGGCAGGTTATCGCCGT	ACGGCGATAACCTGCCGAAGGTCC
	1844	AGTAAGAAGAGGCAGGCCCCACCT	AGGTGGGGCCTGCCTCTTCTTACT
5	1845	AACGGCTCCCCGTCGTA CTGCTTA	TAAGCAGTACGACGGGGAGCCGTT
	1846	CCTATACCGTCGTGGTTCACGTT	AACGTGGAACCACGACGGTATAGG
	1847	CCGCGCAGGCGCTAATACTCAAGG	CCTTGAGTATTAGCGCCTGCGCGG
	1848	AAATGGGCCAGTGAAATCCTTGGT	ACCAAGGATTTCACTGGCCCATTT
	1849	ACGGTTTCGAATACTGCTGGGCAG	CTGCCCAGCAGTATTCGAAACCGT
10	1850	CCGCTTGAGGTT CAGGTCAGAGCT	AGCTCTGACCTGAACCTCAAGCGG
	1851	ATCGTGCCCGAAGACACTTAAACG	CGTTTAAGTGTCTTCGGGCACGAT
	1852	ACCTGAACCAGGGCGATTGCTTTA	TAAAGCAATCGCCCTGGTTCAGGT
	1853	ACCCTATACGCTGGGCTAAGCGGG	CCCGCTTAGCCCAGCGTATAGGGT
	1854	TGTTTCGCGACTAGAAGCCTTTGC	GCAAAGGCTTCTAGTCGCGAAACA
	1855	GAAGTTGGCGGCTCACCCGTATTA	TAATACGGGTGAGCCGCCAACTTC
15	1856	TGGCTACACCGCTTAGGAGGAACC	GGTTCCTCCTAAGCGGTGTAGCCA
	1857	CCACAGTTGCGTGACTTACATCGC	GCGATGTAAGTCACGCAACTGTGG
	1858	ACTGCCACTGCGTCTGAAGAGTGG	CCACTCTTCAGACGCAGTGGCAGT
	1859	GCGCCAGCAAATTTCTGTGTGGTGT	ACACCACACGAAATTTGCTGGCGC
	1860	TGCCTCCGTCGAGCCGAATAGCCA	TGGCTATTGGCTCGACGGAGGCCA
20	1861	GTACAAACGGGCGCTATTTCTGTCC	GGACGAAATAGCGCCCGTTTGTAC
	1862	GCTTCCCTGGCTCTGAACGGAAAC	GTTTCCGTT CAGAGCCAGGGAAGC
	1863	CGGCTACCCAGGCAGATAAGCTGA	TCAGCTTATCTGCCTGGGTAGCCG
	1864	GGTTGGACCCGACAGGGAATTTCC	GGAAATTCCCTGTGCGGGTCCAACC
	1865	GGGGAATACCCGGCGTTTGTAAATA	TATTACAAACGCCGGGTATTCCCC
25	1866	TGGTTCGGTGAGGTTATGTTCCGGT	ACCGAACATAACCTCACCGAACCA
	1867	TCGGTAGGGTTCAGTCGCTGAGGA	TCCTCAGCGACTGAACCCTACCGA
	1868	TTCGGAGTGTGCCGGTGCTAGTAC	GTACTAGCACCGGCACACTCCGAA
	1869	TCGTA CTGGAATGATGGCCGGGCC	GGCCCGGCCATCATTCCAGTACGA
	1870	TCCGTCGACCGTCCAGCGAAGTTT	AACTTCGCTGGACGGTTCGACGGA
30	1871	AGGGAATATAACAACACCGCGCAC	GTGCGCGGTGTTGTTATATTCCCT
	1872	ATGTCCCGGAAACAGCTACCTCA	TGAGGTAGCTGGTTTCCGGGACAT
	1873	ACCAGCGACTTAGATAGCCGTCCG	CGGACGGCTATCTAAGTCGCTGGT
	1874	GGAAAACCTCCTTTGCGTCAACCA	TGGTTGACGCAAAGGAGGTTTCC
	1875	ACGTGCGTGCATACCCAAGAGGAC	GTCCTCTTGGGTATGCACGCACGT
35	1876	ACGCCACTTTCCCTAGAACCAACG	CGTTGGTTCTAGGGAAAGTGCGGT
	1877	CGAAGTACGCAATAGTGCCACCCT	AGGGTGGCACTATTGCGTACTTCG
	1878	GATCCCGGCGGATCACCTATCAAT	ATTGATAGGTGATCCGCCGGGATC
	1879	AGAAAGCGACCGTTTCAGGCTAGC	GCTAGCCTGAAACGGTCGCTTTCT
	1880	CGCTCCCTTTCATAGTCTCTCCG	CGGAGAGGACTATGAAAGGGAGCG
40	1881	GTGGGTGGTCATAACGACAGCAGA	TCTGCTGTCGTTATGACCACCCAC
	1882	CTGGAGGCTGCATCGTTCTGTAACA	TGTTACGAACGATGCAGCCTCCAG

	1883	CACCATGAGTTTCGGAGCGAGGAT	ATCCTCGCTCCGAAACTCATGGTG
	1884	CAAGCTGCGTTCGATGAGAGATTG	CAATCTCTCATCGAACGCAGCTTG
	1885	CCTGGGAGCAATGACCGCTCTGGT	ACCAGAGCGGTCATTGCTCCCAGG
5	1886	TCCGGCGCTCTACCAAGATGAGAC	GTCTCATCTTGGTAGAGCGCCGGA
	1887	CGACCGCGTCGCGTATACTATCCG	CGGATAGTATACGCGACGCGGTCG
	1888	AACATTCGCTAGTGGGGTCCAACA	TGTTGGACCCCACTAGCGAATGTT
	1889	TGTATGATCATCCGACCGAGCAGC	GCTGCTCGGTCGGATGATCATACA
	1890	AGTGCGCCGAGAGGGTGAATAGAC	GTCTATTACCCCTCTCGGCGCACT
10	1891	AGGCTTGTTCTGGACCAGCACCAT	ATGGTGCTGGTCCAGAACAAGCCT
	1892	GGGGCCACATAAAGAATTCCGAAC	GTTTCGGAATTCTTTATGTGGCCCC
	1893	TGGTGAAGATAAATCCGCATGGCA	TGCCATGCGGATTTATCTTCACCA
	1894	ATTTCCACCACGCTCTTGCCAAAT	ATTTGGCAAGAGCGTGGTGGAAT
	1895	CGCGTAAAGCTGTCACCGATGACC	GGTCATCGGTGACAGCTTTACGCG
15	1896	TCCCCAACCGGTAACAACAGCGAC	GTGCTGTTGTTACCGTTGGGGA
	1897	CCTCTGCTCGCCTTACACCCATGG	CCATGGGTGTAAGGCGAGCAGAGG
	1898	CAAGCTGCTCCTGTGCTGAAGGGC	GCCCTTCAGCACAGGAGCAGCTTG
	1899	AAACGAACGATGGTCGGTAGACCG	CGGTCTACCGACCATCGTTCGTTT
	1900	TCAGTTCGATGGCTATTGCGCCTC	GAGGCGCAATAGCCATCGAACTGA
20	1901	GGCTCTCAACGGACGCAAATCATA	TATGATTGCGTCCGTTGAGAGCC
	1902	AGTAGAGTGTTGCGGCTGCCGATC	GATCGGCAGCCGCAACACTCTACT
	1903	AGACACTAGACCGCCGTGACCTGA	TCAGGTCACGGCGGTCTAGTGTCT
	1904	ACCGAGCACCGAATTTCTTGTCC	GGACAAGGAAATTCGGTGCTCGGT
	1905	CCGTGGCCAAGATACGAACGAATT	AATTCGTTCTGTATCTTGCCACGG
25	1906	CCTCCTACAGCATCCACATGAGGG	CCCTCATGTGGATGCTGTAGGAGG
	1907	CACTCGGCAAATACGTATGCGCAT	ATGCGCATACGTATTTGCCGAGTG
	1908	ACCGAGTTGAAGCACGAATTTGGG	CCCAAATTCGTGCTTCAACTCGGT
	1909	GACCACCTCGGAAGATCGTTCTGC	GCAGAACGATCTTCCGAGGTGGTC
	1910	TCAACTGGGCAAACGAAGAGCACA	TGTGCTCTTCGTTTGCCAGTTGA
30	1911	GCTTAGCCTCACACGTGCATACCA	TGGTATGCACGTGTGAGGCTAAGC
	1912	CTGCGGTCTCCAAGTACCATTTCG	CGAAATGGTACTTGAGACCGCAG
	1913	GTTCCGTATTACGGCGGCCATAAG	CTTATGGCCGCCGTAATACGGAAC
	1914	ATCGACGCAACCGGATAGTCTCTG	CAGAGACTATCCGGTTGCGTCGAT
	1915	CGCAGATAAACCGGCATCTTTCAG	CTGAAAGATGCCGGTTTATCTGCG
35	1916	ACCTGCCAATACGGGTCTACGGTT	AACCGTAGACCCGTATTGGCAGGT
	1917	ACACCTGTTGCCATGCTGATCCGT	ACGGATCAGCATGGCAACAGGTGT
	1918	AAACTGTCTACTGCGCAATTCGCG	GCGGAATTGCGCAGTAGACAGTTT
	1919	GCAACTAGCCCGTGCTAGGATCGT	ACGATCCTAGCACGGGCTAGTTGC
	1920	TCGTAGTGGTGGATTGTTGTGCGT	ACGCACAACAATCCACCACTACGA
40	1921	GGCTTACTCCTCAATTGCGACACG	CGTGTCGCAATTGAGGAGTAAGCC
	1922	CACGACTCCCTGCCAGATTTGATT	AATCAAATCTGGCAGGGAGTCGTG
	1923	CTTAGACGTGCGCAATGTCACGTC	GACGTGACATTGCCGACGTCTAAG

	1924	CTCAGAGCACAATCTGCCCTGCCT	AGGCAGGGCAGATTGTGCTCTGAG
	1925	GCTAGGAAAGTCGGCATTTCATGGG	CCCATGAATGCCGACTTTCCTAGC
	1926	AAAGCCCCAAAATTCGCCTAACC	GGTTAGGCGGAATTTTGGGGCTTT
5	1927	GCGCAACGCTAAGGGACTATCAAG	CTTGATAGTCCCTTAGCGTTGCGC
	1928	CGTCCGCTGGGATGAGTCTCCTGC	GCAGGAGACTCATCCCAGCGGACG
	1929	ACAGGCCTCGTGATTGGTGTGGGT	ACCCACACCAATCACGAGGCCTGT
	1930	CATTCTCCTTCCGGGACCACGCCT	AGGCGTGGTCCCGGAAGGAGAAATG
	1931	TCGGAGTTGACCAAGCTCAGTGCG	CGCACTGAGCTTGGTCAACTCCGA
	1932	ACGCGCCACTGCAATTGCAAACAC	GTGTTTGCAATTGCAGTGGCGCGT
10	1933	AGTTCATGGAGCCGGCGTATTGTT	AACAATACGCCGGCTCCATGAACT
	1934	ACGTTTAATGCGGGGCCCCGCCTAC	GTAGGCGGGCCCCGCATTAAACGT
	1935	TGAGGCTTTAGCCTACGCGCAGGT	ACCTGCGCGTAGGCTAAAGCCTCA
	1936	CAGCGTTATGAGCGCGGAGTTTAT	ATAAACTCCGCGCTCATAACGCTG
	1937	GTCCACGTGACCACGGATAGTTGG	CCAACATCCGTGGTCACGTGGAC
15	1938	GATTATGCTCCTACGCCTGCTCCG	CGGAGCAGGCGTAGGAGCATAATC
	1939	TCGTCAAGGGCATGATGTGTGGGA	TCCCACACATCATGCCCTTGACGA
	1940	GATGGACCGCCAAAGACACCTTGA	TCAAGGTGTCTTTGGCGGTCCATC
	1941	TACACGAGGATGGGGTCAAGCTTT	AAAGCTTGACCCCATCCTCGTGTA
	1942	ACACGCACAAAACGTTTGAAAGGC	GCCTTTCAAACGTTTTGTGCGTGT
20	1943	GTTATCGTGGGCCGATGGTACTGA	TCAGTACCATCGGCCACGATAAC
	1944	ACATGACCGTATCCGCCTGCTTCG	CGAAGCAGGCGGATACGGTCATGT
	1945	GAAGGCGAACCCTGAACTACGC	GCGTAGTTTCAGTGGTTCGCCTTC
	1946	TGACTTTTGCAACGGGTGGAACCA	TGGTTCCACCCGTTGCAAAAGTCA
	1947	TGAATTCGTAGGTTTTGGGTGCGG	CCGCACCCAAAACCTACGAATTCA
25	1948	AGCATTATGAAGCGGCCATTGCG	CGCAATGGCCGCTTCATAAATGCT
	1949	TGCTCCTCGCGTTGGTACCGTGAG	CTCACGGTACCAACGCGAGGAGCA
	1950	CGCAGCAAGAAACAGCAACTGTTG	CAACAGTTGCTGTTTCTTGCTGCG
	1951	AGACGCTTGGAGTGAAAACCTCGGA	TCCGAGTTTTCACTCCAAGCGTCT
	1952	CATTCTGATAGTATGCCCCAAATGGA	TCCATTTGGGGCATTCTACGAATG
30	1953	CCAGAAGGTTCCGGGACCCGTCGTG	CACGACGGGTCCCGAACCTTCTGG
	1954	GAGAAGCCGGTTCTCAGAGCACAT	ATGTGCTCTGAGAACCGGCTTCTC
	1955	TTGCGTTGCAAGATATCTGGCCCCG	CGGGCCAGATATCTTGCAACGCAA
	1956	GGGTTGCATGTTTCAGGCAAGACGA	TCGTCTTGCCTGAACATGCAACCC
	1957	CTCACGAAGGTGACATATCACGCC	GGCGTGATATGTCACCTTCGTGAG
35	1958	GCCCGAGATACGGGTTCAAAAAGA	TCTTTTTGAACCGTATCTCGGGC
	1959	CATCTTCGCGCTTCTTCACTCCGC	GCGGAGTGAAGAAGCGCGAAGATG
	1960	TTACACGGTAAGCGTACGGCCGCC	GGCGGCCGTACGCTTACCGTGTA
	1961	ACCTTCGGACAATGTGGCGTTTCGC	GCGAACGCCACATTGTCCGAAGGT
	1962	TGAATGGTTCTGCTAGGCCACAC	GTGTGGGCCTAGCAGAACCATTCA
40	1963	CACGCCTGTCTGACATATGGATGC	GCATCCATATGTCAGACAGGCGTG
	1964	CGCCTCAACCCAATCTGAGAACGT	ACGTTCTCAGATTGGGTTGAGGCG

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1965	TTACGCTTACTGCGAGCTGGGTCC	GGACCCAGCTCGCAGTAAGCGTAA
1966	GGCTTGTGGGGCAATACGCATCTT	AAGATGCGTATTGCCCCACAAGCC
1967	CACTCTCCTTTGGATGCGGAACAA	TTGTTCCGCATCCAAAGGAGAGTG
1968	GACCAGCCATCACGTAACGGCCCT	AGGGCCGTTACGTGATGGCTGGTC
1969	AGGAACCGGATGTGGTTATGGAGC	GCTCCATAACCACATCCGGTTCCT
1970	ATCCATGGGCAACTGAGCCTATGC	GCATAGGCTCAGTTGCCCATGGAT
1971	GGAACAGCACTTGTTACCGCCAC	GTGGGCGGTAACAAGTGCTGTTCC
1972	TGGCTCGCTTCAAGCCTGTTTGCT	AGCAAACAGGCTTGAAGCGAGCCA
1973	CAAACGTGAGGTCATGACCACCAT	ATGGTGGTCATGACCTCACGTTTG
1974	ACCGATGTCTTGAAGTCCGGAGGT	ACCTCCGACTTCAAGACATCGGT
1975	CGAAAATGCATGATGATCTCCCT	AGGGGAGATCATCATGATTTTCG
1976	TTTGGTATTCTCGCTGCACCGTTG	CAACGGTGCAGCGAGAATACCAAA
1977	GCGTACTCAACCACATTCCCGACC	GGTCGGAATGTGGTTGAGTACGC
1978	AGCAAACAACAGCGGTCCGAGCAT	ATGCTCGGACCGCTGTTGTTTGCT
1979	GGACTAGGAGCGGGGATAGCTGAG	CTCAGCTATCCCCGCTCCTAGTCC
1980	CCTTAACGAAAACCTGTCGACCGC	GCGGTCGACAGGTTTTCGTTAAGG
1981	CTCGATCGCATAAGCAAGAAACCG	CGGTTTCTTGCTTATGCGATCGAG
1982	CCCGTTGTTTGGGCGACAAAAAGT	ACTTTTGTGCCCCAAACAACGGG
1983	CGGCGGCTCTCGCATGATCTCGTT	AACGAGATCATGCGAGAGCCGCCG
1984	CGGATGGAGAGGAGTCTACGTCCC	GGGACGTAGACTCCTCTCCATCCG
1985	CAGAACAATATCGTGCCTCAACCG	CGGTTGACGCACGATATTGTTCTG
1986	CCTTTGCGCGCTCCGAGTAAGGTA	TACCTTACTCGGAGCGCGCAAAGG
1987	GGAAACGGCACCTATCTGTCGTGA	TCACGACAGATAGGTGCCGTTTCC
1988	CGACCGACAAAACCAATGCCGCC	GGCGGCATTTGGTTTTGTCGGTCG
1989	CCAAGGGTGTGGGAGCTGAAGAGA	TCTCTTCAGCTCCCACACCCTTG
1990	TTAAGTGCGCATAGTCTCGTGGG	CCCACGAGGACTATGCGCACTTAA
1991	GCCTGGTGGGGTAAGTCATGATGC	GCATCATGACTTACCCACACAGGC
1992	GAGCAGCAGATTGATGCGCTTATG	CATAAGCGCATCAATCTGCTGCTC
1993	TGCGCCAACTTCCGGAATATTTGC	GCAAATATTCCGGAAGTTGGCGCA
1994	AACCCCATCATGAAATGCTCTCCG	CGGAGAGCATTTCATGATGGGGTT
1995	GTCCAACGGTACTGGCGTGATGTT	AACATCACGCCAGTACCGTTGGAC
1996	ACTCGGCTGATCGTGAGATGGTGA	TCACCATCTCACGATCAGCCGAGT
1997	ATTCGTGGGCGCATCTCGGAATGT	ACATTCCGAGATGCGCCCACGAAT
1998	TCCCGTCCTGTAATCCAGGGAACA	TGTTCCCTGGATTACAGGACGGGA
1999	CTTCGCTGCACCTACATTGCGCCA	TGGCGCAATGTAGGTGCAGCGAAG
2000	GCGTGTAGATGACTGTGCTTTGGG	CCCAAAGCACAGTCATCTACACGC
2001	CTATGGTATCGAGACATCGGCGGA	TCCGCCGATGTCTCGATACCATAG
2002	CCTCGTACTCGTCGTATGCACAA	TTGTGCATACGACGGAGTACGAGG
2003	TGGTGCGTCCGTAGTGCCTGCACT	AGTGCAGGCACTACGGACGCACCA
2004	CGCGATCCTAGTTGAAAGCTTTGC	GCAAAGCTTTCAACTAGGATCGCG
2005	ACGATCCAGGTGTTGGGCACTAAG	CTTAGTGCCCAACACCTGGATCGT



	2006	CCAATCTAGGATACACCACGCCCG	CGGGCGTGGTGTATCCTAGATTGG
	2007	GATACGTGGGGTATAGGCGGGCCC	GGGCCCCGCTATACCCACGTATC
	2008	CATGGAACAAACCGTCGTAGGGGA	TCCCCTACGACGGTTTGTTCATG
	2009	ACACTCGCGCAGTATTCGAGTCGT	ACGACTCGAATACTGCGCGAGTGT
5	2010	CTCAGTCTCGAAGGTGATCCGACC	GGTCGGATCACCTTCGAGACTGAG
	2011	TCCCAATCCCCGTGGTATCGTCGT	ACGACGATACCACGGGGATTGGGA
	2012	AATCAACGTAGTTCCGGTGGTCCG	CGGACCACCGGAACACGTTGATT
	2013	CTTAACAACCCAGGGGTTTGGGCT	AGCCCAAACCCCTGGGTTGTTAAG
	2014	CTACCGCTGCATGGCGTTAGATTG	CAATCTAACGCCATGCAGCGGTAG
10	2015	TTATTGGTGGCGGACGGAGTGAGT	ACTCACTCCGTCCGCCACCAATAA
	2016	TAAAGGGTGAACCTCAACCGCGTGA	TCACGCGGTTGAGTTCACCCTTAA
	2017	TTTGATTGAAACGCTGCGCACTAC	GTAGTGCGCAGCGTTTCAATCAAA
	2018	TCATGTGTAGGTGCGCGCCGTCAC	GTGACGGCCGCGACCTACACATGA
	2019	CTCCGAACCTTCTGGGCCTCTTTT	AAAAGAGGCCCCAGAAGGTTCCGAG
15	2020	CTGTTGCCCATTTGGCCCGACACTC	GAGTGTCGGGCCAATGGGCAACAG
	2021	CACGATCGCTGAGCAACACATCAC	GTGATGTGTTGCTCAGCGATCGTG
	2022	CGGATCATAAGCGTCCGCCTTCGT	ACGAAGGCGGACGCTTATGATCCG
	2023	AGGTAAACGCAACATGTGATCCGC	GCGGATCACATGTTGCGTTAACCT
	2024	GGGAAAAACAGCTAAGCCTTGCGA	TCGCAAGGCTTAGCTGTTTTTCCC
20	2025	ACTTATTGCCGGGATCCGTACACA	TGTGTACGGATCCCGGCAATAAGT
	2026	TGCGGTCTGAAAGGAAGGGAGGG	CCCTCCCTTCCTTTCCAGACCGCA
	2027	GCTGCCACCTGGACATCGCATACA	TGTATGCGATGTCCAGGTGGCAGC
	2028	GCAGGCATGACAGTGGCGTAGTAC	GTACTACGCCACTGTCATGCCTGC
	2029	GCGGCCCTGATGGTTTGGCTGAGC	GCTCAGCCAAACCATCAGGGCCGC
25	2030	TCCCATTAGTCCCCTCCATCAC	GTGATGGAGGGGACTAAATGGGGA
	2031	GCAACACAAATGCGAGCGTAGGAG	CTCCTACGCTCGCATTTGTGTTGC
	2032	GGCGTTTGTATTGAGCCACGTAG	CTACGTGGCTCGAATACAAACGCC
	2033	GGTAACGTCGCACGTGGAATTCCG	CGGAATTCCACGTGCGACGTTACC
	2034	ACTTCACAACGCTCCGTTGGACAC	GTGTCCAACGGAGCGTTGTGAAGT
30	2035	CCGAATTATAAAGCGCAAGGCACA	TGTGCCTTGCCTTTATAATTCCG
	2036	GGACCCGATAAGACTCTGACGCCG	CGGCGTCAGAGTCTTATCGGGTCC
	2037	ACCCGTTTCTCGTAGGAACCTGCT	AGCAGGTTCTACGAGAAACGGGT
	2038	CACGTTCCGACTGTATCTGGTTGCC	GGCAACCAGATACAGTCGAACGTG
	2039	CCTCGGATGGGCCCATGACCTTGA	TCAAGGTCATGGGCCCATCCGAGG
35	2040	GGACGCCTGCTGTAGGGGTTTGAT	ATCAAACCCCTACAGCAGGCGTCC
	2041	CTCGAGCGTGGGCTAAAAGAGCAT	ATGCTCTTTTAGCCACGCTCGAG
	2042	TTTACTTCTTAGGGCGCGTTTGGG	CCCAAACGCGCCCTAAGAAGTAAA
	2043	ACCACCAACATAGCGCGCACTAGT	ACTAGTGC GCGCTATGTTGGTGGT
	2044	TGGTTACACGGCAGCCCGGTAAAG	CTTACGCGGGCTGCCGTGTAACCA
40	2045	TTATGGTACGTTGCTGCGTGCGGG	CCCGCACGCAGCAACGTACCATAA
	2046	ACCGCGGATCTAACGAATCCCAT	AATGGGATTGTTAGATCCGCGGT

2047	CATGATCCCGCCCTTAGGTTAAGC	GCTTAACCTAAGGGCGGGATCATG
2048	TACCGCTTCAAAGGGTTGCCGAAT	ATTCGGCAACCCTTTGAAGCGGTA
2049	GCACCGCGTCAATATTACCGAGGA	TCCTCGGTAATATTGACGCGGTGC
2050	GTGTCGCGGCTTTACAGAAGGAGA	TCTCCTTCTGTAAAGCCGCGACAC
2051	GCAAGCCATACCGCAATAAACTCG	CGAGTTTATTGCGGTATGGCTTGC
2052	ATGAGGTCGTGCTGCGTTCACGAG	CTCGTGAACGCAGCACGACCTCAT
2053	CGAGACTAGTGCCGATGCAGGGTA	TACCCTGCATCGGCACTAGTCTCG
2054	GCCTCATCATAGACGCTGGATGCA	TGCATCCAGCGTCTATGATGAGGC
2055	GACAGGCGTCGGTAAGCTCTCAAG	CTTGAGAGCTTACCGACGCCTGTC
2056	GCTACGAATCTTCCCTGTCGCCAC	GTGGCGACAGGGAAGATTCTGTAGC
2057	TTTGGCAGAACGTACCAAGTGGGGT	ACCCCACTGGTACGTTCTGCCAAA
2058	GGACAATAAGCACCGGAGAATGCG	CGCATTCTCCGGTGCTTATTGTCC
2059	TCATGAACCTTCTGATGCCGCGAA	TTCGCGGCATCAGAAGGTTTCATGA
2060	CGCCGCATTACCTTAAAAACGTGC	GCACGTTTTTAAGGTAATGCGGCG
2061	ACGAGTCCAACCGCCTCATTGATT	AATCAATGAGGCGGTTGGACTCGT
2062	GCGAAGAGTTGCTACTCTTCCGCC	GGCGGAAGAGTAGCAACTCTTCGC
2063	CGTCGGCAACAATCTTTTCGTGA	TCACGAAAAAGATTGTTGCCGACG
2064	AATCCTGTGCACCCGTGAGACGCG	CGCGTCTCACGGGTGCACAGGATT
2065	AACCTATATGCATCAACGCGAGCC	GGCTCGCGTTGATGCATATAGGTT
2066	GAAC TTGGCAAAACAGCCCGGAAA	TTTCCGGGCTGTTTTGCCAAGTTC
2067	CTCTATGGCCGTTTGCCGTCTGCA	TGCAGACGGCAAACGGCCATAGAG
2068	AGTGCACCGGGTTGTGGACACAAT	ATTGTGTCCACAACCCGGTGCACT
2069	CCTGGCTTTTCACACGCCAAGAAA	TTTCTTGGCGTGTGAAAAGCCAGG
2070	CACTCAGCGTAGCCTGAAGCCTGG	CCAGGCTTCAGGCTACGCTGAGTG
2071	GAATTATCGACCGCAGCGGTGTGCG	CGACACCGCTGCGGTGCGATAATTC
2072	GTGACATCACATGGTGGCCGAGCG	CGCTCGGCCACCATGTGATGTCAC
2073	AGCACCTTGCCGAGTCACCAAGTGA	TCACTGGTGA CTGCGCAAGGTGCT
2074	TAGGTTGCAGGAATGGTGGGCACC	GGTGCCCACTTCCTGCAACCTA
2075	GTCCCATACGTGTGGTACGCGGAT	ATCCGCGTACCACACGTATGGGAC
2076	TCGGATACTCTCGCGTGCCACGGG	CCCGTGGCACGCGAGAGTATCCGA
2077	CAACGTTCCGCCCTAAGCCCAAAT	ATTTGGGCTTAGGGGCGAACGTTG
2078	GTTAGGTCACCGCGGCATATCCTA	TAGGATATGCCGCGGTGACCTAAC
2079	GTTACCGGCCCTCTACTTGGGTTT	AAACCCAAGTAGAGGCCGGTGAAC
2080	AATCCGCGTCTAGGTCATGTGGTC	GACCACATGACCTAGACGCGGATT
2081	GCTACGCCTCTGGAGGTGGTACCC	GGGTACCACCTCCAGAGGCGTAGC
2082	CAGGGAATGCTACAAAGGGTCAA	TTGGACCCTTTGTAGCATTCCCTG
2083	AAGGGTTAGCTGCCCCGGTTAACAG	CTGTTAACCGGGCAGCTAACCTT
2084	CCTCGCAAGCGCGATATTTATGCC	GGCATAAATATCGCGCTTGCGAGG
2085	GCCTCCCGGTCATGGTCAAGGGAA	TTCCCTTGACCATGACCGGGAGGC
2086	GCTGTTGAGCGGCGACCTGTGCAC	GTGCACAGGTCGCCGCTCAACAGC
2087	CGCTGACTTAGCTCTGATGTGCCG	CGGCACATCAGAGCTAAGTCAGCG

2088	TTCATGGCATTTCATCACGAAGGAA	TTCCTTCGTGATGAATGCCATGAA
2089	TAGTGTTATGCCCCGCGTGTGAATG	CATTCACACGCGGGCATAACACTA
2090	CATGTAAGGGCACGGTCGTGGGCA	TGCCCACGACCGTGCCCTTACATG
2091	CAGGAAGCTCGCTCCGTGATGCAC	GTGCATCACGGAGCGAGCTTCCTG
2092	CCTGCTGATAGCAACCTCACTGCA	TGCAGTGAGGTTGCTATCAGCAGG
2093	ACTACGAGGGGACAGGGTCTAGGCG	CGCCTAGACCCTGCCCCCTCGTAGT
2094	CATAATGTGGGTGCTGACGCCGAT	ATCGGCGTCAGCACCCACATTATG
2095	TAGCGAATCCACACAGAGCCGCTC	GAGCGGCTCTGTGTGGATTTCGCTA
2096	TCGCGAAATCCCTAAATCCTGTGC	GCACAGGATTTAGGGATTTTCGCGA
2097	TGGCACGAATCAAGCCACCAACTC	GAGTTGGTGGCTTGATTTCGTGCCA
2098	GCGGACCGTCTTTGCTATCTGACG	CGTCAGATAGCAAAGACGGTCCGC
2099	AGGCCCCGCTTGTAAATTGGTCAT	ATGACCAATTACAAGGCGGGGCCT
2100	CTGGTCCCATACGCCGCTGACTAG	CTAGTCAGCGGCGTATGGGACCAG
2101	TGCTAACTGCGGCCCTACAGAGTC	GACTCTGTAGGGCCGCGAGTTAGCA
2102	TGGTTTTATGTTTCGGTAGCGTCCG	CGGACGCTACCGAACATAAAACCA
2103	AGCTCAAACCTCTCCACGGGATG	CATCCCGTGGGAGAAGTTTGAGCT
2104	CGCGAAGATAGTGAAATCCGCATC	GATGCGGATTTCACTATCTTCGCG
2105	GAGTGAAACCTCTCGCGGGTTGCA	TGCAACCCGCGAGAGGTTTCACTC
2106	TCGAATGCTCTGCAGTGACGTCAA	TTGACGTCACTGCAGAGCATTCTGA
2107	AGGTGGCAATGATCGACGACCCTG	CAGGGTCGTCGATCATTGCCACCT
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2109	CTTTTGGGGATTAGAGGCCGACAA	TTGTCGGCCTCTAATCCCCAAAG
2110	GGCATAAAGGCTTCCGTTCCCTGTC	GACAGGAACGGAAGCCTTTATGCC
2111	GCGGACCGTAAAGCGGGCAGATAG	CTATCTGCCCCGCTTTACGGTCCGC
2112	TTTCAAGAGTGCATCGAATCCACG	CGTGGATTTCGATGCACTCTTGAAA
2113	CCGGCATCCCTTCTCGCTGTTGCC	GGCAACAGCGAGAAGGGATGCCGG
2114	ACACAGAGACGCGAACGGAGTGCA	TGCACTCCGTTGCGCTCTCTGTGT
2115	AGCGGCATTCTCCCACTCGTTACT	AGTAACGAGTGGGAGAATGCCGCT
2116	GGAGCGTACTGCGCCTCGCAAGTC	GACTTGCGAGGCGCAGTACGCTCC
2117	AAACCCGAATGACACGGCAGATAA	TTATCTGCCGTGTCAATCGGGTTT
2118	AACCAGCGGATCGATAAAACGACA	TGTCGTTTTATCGATCCGCTGGTT
2119	GGTGTCCACCCGTTAACGCCGGTA	TACCGGCGTTAACGGGTGGACACC
2120	AGCGCGACGTGGCTTGCCGTTAAA	TTTAACGGCAAGCCACGTCGCGCT
2121	TCCCACGGCTATAGGTCCAACGAC	GTCGTTGGACCTATAGCCGTGGGA
2122	ATCAACGAACGATGCCGTTAGGTG	CACCTAACGGCATCGTTCGTTGAT
2123	GAGGCTAAGCCGATGGCCGAGGC	GCCTCGGCCATACGGCTTAGCCTC
2124	ACGGTCCGAAATGGTTAGAGGCAC	GTGCCTCTAACCATTTCGGACCGT
2125	ACGCAAACCATTCCTCGAGTAGGC	GCCTACTCGAGGAATGGTTTGCGT
2126	TTACACGCTCGCTATTGGGCCATA	TATGGCCCAATAGCGAGCGTGTA
2127	CTCGGCACGGGTTTAGAACGCCGG	CCGGCGTTCTAAACCCGTGCCGAG
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	2129	AGCACACCGTTATACATGACGGCG	CGCCGTCATGTATAACGGTGTGCT
	2130	AGTCCCTGCCGTTTCGCTCATGGAA	TTCCATGAGCGAACGGCAGGGACT
	2131	GGGCTTATGACCAGTCAGGTTGGA	TCCAACCTGACTGGTCATAAGCCC
5	2132	GGTCACCACACGAGTGCCTGGTCT	AGACCAGGCACTCGTGTGGTGACC
	2133	TTGATCGTGTCTCCCGAAACCCTC	GAGGGTTTCGGGAGACACGATCAA
	2134	ATTGTCGCGATCGGCATTTCTTAA	TTAAGAAATGCCGATCGCGACAAT
	2135	GGGTCCAACGACTTCTCGCTGCTG	CAGCAGCGAGAAGTCGTTGGACCC
	2136	CAAATTCCTTGGGGGCCATAGTGG	CCACTATGGCCCCAAGGAATTTG
10	2137	CCAGAGTATCCGCCGTTAGACGGT	ACCGTCTAACGGCGGATACTCTGG
	2138	TCCTGCAGATCATCTCGTGTCTGG	CCAGACACGAGATGATCTGCAGGA
	2139	TGCGGGAGATTTGAACAAGCTGTA	TACAGCTTGTTCAAATCTCCCGCA
	2140	TTAGACGCCGAGCTAGGCAACGTC	GACGTTGCCTAGCTCGGCGTCTAA
	2141	TTTCGGCAGAATCTCCGATTCAAC	GTTGAATCGGAGATTCTGCCGAAA
15	2142	TGGCGAGCAGACCTACAAGACAGA	TCTGTCTTGTAGGTCTGCTCGCCA
	2143	GGCGACAGACCGGTACATCGGCCA	TGGCCGATGTACCGGTCTGTGCGCC
	2144	TCTAGACCTGCGTTTCGTGGGACC	GGTCCACGAAACGCAGGTCTAGA
	2145	GCCGAGCGTGGTACCATACGTTCA	TGAACGTATGGTACCACGCTCGGC
	2146	TAATCACACCCGCTTTCTGTGGCT	AGCCACAGAAAGCGGGTGTGATTA
20	2147	GGCCGGAGCCATTGGACACTTCTT	AAGAAGTGTCCAATGGCTCCGGCC
	2148	CCTGTAGACCTGCATGGATCGCTG	CAGCGATCCATGCAGGTCTACAGG
	2149	ATCGCCGTTCCCGCAAATAAGCA	TGCTTATTTGCGGGAACGGCGAT
	2150	TGGATCAACGGGGTAGTGAAACG	CGTTTTCACTACCCCGTTGATCCA
	2151	AAGCGACGATGCTTTCTTGAGCTG	CAGCTCAAGAAAGCATCGTCGCTT
25	2152	CACGGGCACGTGTTCTACGCTTGC	GCAAGCGTAGAACACGTGCCCGTG
	2153	ACGGGCTGGGACAAGAGCTAGAAA	TTTCTAGCTCTTGTCCCAGCCCGT
	2154	GGTAACTGGCTCCGCTCTCACATC	GATGTGAGAGCGGAGCCAGTTACC
	2155	ACTCTGGCTGTTGGCGAACGTGAC	GTCACGTTCCGCAACAGCCAGAGT
	2156	GACCGAGGACCAGTCCTTGCTCTC	GAGAGCAAGGACTGGTCTCGGTC
30	2157	AGTAGCTCTTGCGGCCTAACGGCA	TGCCGTTAGGCCGCAAGAGCTACT
	2158	TTCTTGTCCTGGGGGAGAGCAGTG	CACTGCTCTCCCCAGGACAAGAA
	2159	TTAGCAGGGAGGTTGTGCGGCTCAT	ATGAGCCGACAACCTCCCTGCTAA
	2160	AGAACGTGGATTGTACGCTCCGCC	GGCGGAGCGTACAATCCACGTTCT
	2161	CTTCACAGCCTGGAGCCACCAATG	CATTGGTGGCTCCAGGCTGTGAAG
35	2162	GAGATCGATGAAACGCACCAGCGG	CCGCTGGTGCCTTCATCGATCTC
	2163	GGGTCCAGAGTTGGTGTGGGATAA	TTATCCCACACCAACTCTGGACCC
	2164	CCGTCCACCCCAGATAGGAATCAC	GTGATTCTATCTGGGGTGGACGG
	2165	TGCCTCGCTTCTGTGAATCTACGA	TCGTAGATTACAGAAGCGAGGCA
	2166	GATCACAGCGTCCGCGCATAACGG	CCGTTATGCGCGGACGCTGTGATC
40	2167	ATGACGCCTTACATGACGCACCTT	AAGGTGCGTCATGTAAGGCGTCAT
	2168	GCGTGGAATAACGCCCTTAGTTCA	TGAACTAAGGGCGTTATTCCACGC
	2169	GGTCTACCATTTCTCGCCCGACCG	CGGTCCGGGCGAGAAATGGTAGACC

	2170	ACACCTCTCTGGCGTAGACGCTCA	TGAGCGTCTACGCCAGAGAGGTGT
	2171	GTAGAGGTGCTCAGGACTCGTCGC	GCGACGAGTCGTGAGCACCTCTAC
	2172	GTAAGCAGGAGGCGAAGGCGCGAA	TTCGCGCCTTCGCCTCCTGCTTAC
5	2173	TCTAAGGGCCGTTTCAATCGACCT	AGGTCGATTGAAACGGCCCTTAGA
	2174	AACCTGATTTCAGGGTCAGCCCGA	TCGGGCTGACCCTGAAATCAGGTT
	2175	GTCACGCGATTGGCCCACCTATTA	TAATAGGTGGGCCAATCGCGTGAC
	2176	ACGATGCCGCGCATGTAACCTAGT	ACTAGGTTACATGCGCGGCATCGT
	2177	TGAGAGATGTCTCGTCAACGCCTG	CAGGCGTTGACGAGACATCTCTCA
10	2178	GCATATCTCGCGGTGACAGACGAA	TTCGTCTGTCACCGCGAGATATGC
	2179	GACCCAACGTCGAAATTGTGCGAT	ATCGCACAATTTGACGTTGGGTC
	2180	TGAAAATCGGGGCATCTAGTTTGG	CCAAACTAGATGCCCCGATTTTCA
	2181	CCGCGAAAAGGATTTGTGTACGCA	TGCGTACACAAATCCTTTTCGCGG
	2182	CATTCCATTTATCCGCAGTTCGCT	AGCGAACTGCGGATAAATGGAATG
15	2183	CCTGTCTGTGCGAGCCAGCGTCTAT	ATAGACGCTGGCTCGACAGACAGG
	2184	TCAGCGCGGCTAAACAAGTTATGC	GCATAACTTGTTTAGCCGCGCTGA
	2185	ACGCCTACGAACGACCCAAGAGAG	CTCTCTTGGGTCGTTCTGAGGCGT
	2186	TGCGCATCTACCATTGTGTGGATC	GATCCACACAATGGTAGATGCGCA
	2187	AAGTCCGCGCTCGCTCCTGTAATA	TATTACAGGAGCGAGCGCGGACTT
	2188	GCTGGGTCATTGCTCGAGTAACCA	TGGTTACTCGAGCAATGACCCAGC
20	2189	TGGAGCGTTCTGGCAATGACCGAC	GTCGGTCATTGCCAGAACGCTCCA
	2190	CAAGTCAATTCTTGGCCAATTCGG	CCGAATTGGCCAAGAATTGACTTG
	2191	CGTTCATGCAAGGATCCAGGTTA	TAACCTGGGATCCTTGCATGAACG
	2192	ATGCCAATAGAAGCTGGGGATGCT	AGCATCCCAGCTTCTATTGGCAT
	2193	CCTAACTCTCCCTTGAGGCCGTTT	GAACGGCCTCAAGGGAGAGTTAGG
25	2194	ATCTCGGCGAAGGTTCCAAACATT	AATGTTTGGAACCTTCGCCGAGAT
	2195	GCGACAGATTACGCTGCGGTTTTT	GAAAACCGCAGCGTAATCTGTGCG
	2196	AAGCCAGACGGCCAACACGTTAC	GTAACGTGTTGGCCGTCTGGGCTT
	2197	TCAAGTTCAAATCACATCCCGTGG	CCACGGGATGTGATTTGAACTTGA
	2198	GATTGTGCTTCTGTCTGTGAGGCG	CGCCTCACAGACAGAACGACAATC
30	2199	ACCGAACTATGTTCCGGCATGGCA	TGCCATGCCGGAACATAGTTCGGT
	2200	CGTCATCGGGTGTGCAATGCCGTT	AACGGCATTGCACACCCGATGACG
	2201	CGGACGGAGTCACGTTTGTGCACT	AGTGCAACAAACGTGACTCCGTCCG
	2202	TAAACAAGTCGTGTGCCCTTTGCCG	CGGCAAAGGCACACGACTTGTTTA
	2203	TAATTACTGGCCTGTGGAGCAGGC	GCCTGCTCCACAGGCCAGTAATTA
35	2204	GGAGCGGCCCGAATGGTGCTCTTA	TAAGAGCACCATTTCGGGCCGCTCC
	2205	ACTAAGCAAGGCTTGATGTGCGT	ACGCACATCCAAGCCTTGCTTAGT
	2206	GGCAGCTCAGCGGCAGTACGCTAC	GTAGCGTACTGCCGCTGAGCTGCC
	2207	GCGAGGCGAATTATCCGCGGATTT	AAATCCGCGGATAATTGCGCTCGC
	2208	CATACGACACACCTTGGGGTGCTA	TAGCACCCCAAGGTGTGTCGTATG
40	2209	TGCTTGGGCTTTAAACCCCGTTTT	AAAACGGGGTTTAAAGCCCAAGCA
	2210	CCGTTTGAAAACGCAATATCGG	CCGATATTTGCGTTTTCCAACCGG

	2211	AAACTAGCTAGCCGCACCCGCAAG	CTTGCGGGTGCGGCTAGCTAGTTT
	2212	GTTGTTCCACCAGTGATCACGCAG	CTGCGTGATCACTGGTGAACAAC
	2213	GCCGCTGACAAGATGATCATCGTT	AACGATGATCATCTTGTCAGCGGC
	2214	CTTTCATAAAGCCAACCGATGCC	GGGCATCGGTTGGCTTTATGAAAG
5	2215	CTGACTGCATCTCGAAAGCGGGTG	CACCCGCTTTCGAGATGCAGTCAG
	2216	ATTTCTTCGAGAATCGGCCACGT	ACGTGGCCGATTCTCCGAAGAAAT
	2217	CATTTGCGGCCCTAGCTACTGCGC	GCGCAGTAGCTAGGGCCCCGAAATG
	2218	CCGATCCCGCACATCCGTATCCTG	CAGGATACGGATGTGCGGGATCGG
	2219	TATCACCGGGAGCGTCTTATCGTG	CACGATAAGACGCTCCCGGTGATA
10	2220	TAGGGCTCGTGACCGATTAGAGG	CCTCTAATCGGTGCACGAGCCCTA
	2221	GCGTGGCACTCGCTTGTCTAGGTA	TACCTAGACAAGCGAGTGCCACGC
	2222	CTCAACGAACTCAAGGGCCGCTAC	GTAGCGGCCCTTGAGTTCGTTGAG
	2223	AGCCTGGTATCGACCAATCCTGCA	TGCAGGATTGGTCGATACCAGGCT
	2224	TACGCGTTCTAGTTGGCCGGATCC	GGATCCGGCCAACTAGAACGCGTA
15	2225	TTTATGGGTTTGTGCCTGATGGGT	ACCCATCAGGCACAAACCCATAAA
	2226	GGGACCCCTAGCAACGTCACCTTA	TAAGGTGACGTTGCTAGGGGTCCC
	2227	CTGCCTCCCCAGGAGTCATTGGAT	ATCCAATGACTCCTGGGGAGGCAG
	2228	AACCCCGCAAGACCAGTACCAATC	GATTGGTACTGGTCTTGCGGGGTT
	2229	GGTCACATACGCGCTAAAAAGCGC	GCGCTTTTTCAGCGGTATGTGACC
20	2230	AAATGGCTCCGACCAGTTAGGGAC	GTCCCTAACTGGTCGGAGCCATTT
	2231	AACGCGGCACGCTTAAAGGTGCAT	ATGCACCTTTAAGCGTGCCGCGTT
	2232	GATCGCACGCCGATTAACCTTACA	TGTAAGGTTAATCGGCGTGCGATC
	2233	CCTCCTGATTGGGAGTGCGGAATT	AATTCCGCACTCCCAATCAGGAGG
	2234	CGGAGGGTAATAGGCTCCTCTGCG	CGCAGAGGAGCCTATTACCCTCCG
25	2235	ACAAGAACTGGACATTACCGCGGG	CCCGCGGTAATGTCCAGTTCTTGT
	2236	TGTCGTCTTAAAGGCCTTTGTGCG	CGCACAAAGGCCTTTAAGACGACA
	2237	GGTGACCATGTGGCGTTTTAGCTT	AAGCTAAAACGCCACATGGTCACC
	2238	CACGGTTGCGCACGGTACCAGAAC	GTTCTGGTACCGTGCGCAACCGTG
	2239	CCTTTATTGTTTGGTCCCCTGCCC	GGGCAGGGGACCAACAATAAAGG
30	2240	GTGCGCCTGCATTCTACCGTCAAT	ATTGACGGTAGAATGCAGGCGCAC
	2241	GTTTACGTTGATGGCTTGCCGCCG	CGGCGGCAAGCCATCAACGTAAAC
	2242	CCGTGCGTGGTAGGACGTGAATGT	ACATTCACGTCTACCACCGACGG
	2243	TGATCGCCCCAGAATCCCTGTGCT	AGCACAGGGATTCTGGGGCGATCA
	2244	AAGCAGCCAAAAATCGGTTGCTTT	AAAGCAACCGATTTTGGCTGCTT
35	2245	CGACGGGACTTAGTAGCAGGGCCT	AGGCCCTGCTACTAAGTCCCGTCG
	2246	CCGATTGCGGAAACGACCAAGTAG	CTACTTGGTCGTTTCGCGAATCGG
	2247	CCACCCCAACTCCAATCTTTCTCA	TGAGAAAGATTGGAGTTGGGGTGG
	2248	GTGCAGTAGACGACTACCGGCGTC	GACGCCGGTAGTCGTCTACTGCAC
	2249	TTGCCCCATCGTATCAAGCAATTC	GAATTGCTTGATACGATGGGCGAA
40	2250	GAATCGCGACTACCCGTGCGGTCA	TGACCCGACGGGTAGTCGCGATTTC
	2251	CCAGCACTCGCCATCGGTTATAAT	ATTATAACCGATGGCGAGTGCTGG

	2252	CGAACCGTAGAACTCCGGTCGGTG	CACCGACCGGAGTTCTACGGTTCG
	2253	GCACCATGACAGAGCCCCAGGATG	CATCCTGGGGCTCTGTGTCATGGTGC
	2254	TGGGCTACCGCAGAATAAGGGTGA	TCACCCTTATTCTGCGGTAGCCCA
5	2255	TGGCCTGTCGTGTCTGAAGGAAACA	TGTTTCCTTCGACACGACAGGCCA
	2256	GCCTCACCGATAGCGAGCGTTTGC	GCAAACGCTCGCTATCGGTGAGGC
	2257	GTGCGCGCCGGCTAAAACGAGACA	TGTCTCGTTTTAGCCGGCGCGCAC
	2258	CCGCAGACGAGTTTCTTGTGACAG	CTGTCACAAGAACTCGTCTGCGG
	2259	GTTTCGCAATCGCGTGTAGGAAGC	GCTTCCTAGCACGCGATTGCGAAC
10	2260	TGTTGTACACATGCATCCGGTGAA	TTACCCGGATGCATGTGTACAACA
	2261	CACTGAACACGATATAAGGGCGCG	CGCGCCCTTATATCGTGTTCACTG
	2262	CGCGATGGTTCTTAGCAAGACGAT	ATCGTCTTGCTAAGAACCATCGCG
	2263	TACACCAAGGAAGAAATGGGGACG	CGTCCCCATTTCTTCCTTGGTGTA
	2264	CGTGCCTTGCGTTTTAGGTGCAGC	GCTGCACCTAAAACGCAAGGCACG
15	2265	GTCGTTTGTCTGGGCATTAACGGC	GCCGTTAATGCCAGACAAACGAC
	2266	CAGGCTCTCGTTCGGTACAAACGT	ACGTTTGTACCGAACGAGAGCCTG
	2267	CGGACACTGTTTCACCAGAACCCA	TGGGTTCTGGTGAACAGTGTCCG
	2268	TACCCATGATGCGGAAGAAGCGTA	TACGCTTCTTCCGCATCATGGGTA
	2269	CTGTCCCTTAAGCGGATGAGAACCG	CGGTTCTCATCCGCTTAAGGACAG
20	2270	CGGGAGATGAGAACGGTTTTGTGC	GCACAAAACCGTTCTCATCTCCCG
	2271	TAGATCGCGACTGTACTCAGGCCG	CGGCCTGAGTACAGTCGCGATCTA
	2272	TAAACAGTTCGCGCGACTGTCGT	ACGACAGTCGCGGAACTGTTTTA
	2273	CGAGGAGCTCCACATAAGCCCAAT	ATTGGGCTTATGTGGAGCTCCTCG
	2274	TGGCTAGGGATGGGGAATCATCTT	AAGATGATTCCCATCCCTAGCCA
25	2275	AGGATTGGGTGCCTGGATGCATTG	CAATGCATCCAGGCACCCAATCCT
	2276	TGTATCTACCGGCTGAAGCAGGT	ACCTGCTTCAGGCCGGTAGATACA
	2277	TCCCTACGCGCATGACTCGCTTAC	GTAAGCGAGTCATGCGCGTAGGGA
	2278	TGGTCGATCACCTGTGACAGACGC	GCGTCTGTCACAGGTGATCGACCA
	2279	TGGGGGTAGTCCATGCATCAATTG	CAATTGATGCATGGACTACCCCA
30	2280	CCCTGCCAGGATTACTATTCCGGA	TCCGGAATAGTAATCCTGGCAGGG
	2281	TCCCGCACGGGGAATTTAAGTAGA	TCTACTTAAATTCCCCGTGCGGGA
	2282	GTGATGTGCAGGAATTCTGTGCGC	GCGACAGAAGTTCCTGCACATCAC
	2283	ATTTAGGCATGCATGCGCTTCTCA	TGAGAAGCGCATGCATGCCTAAAT
	2284	TTCGGCGCTAGTGGACGCCGTCAA	TTGACGGCGTCCACTAGCGCCGAA
35	2285	GAGCTTCATCTCATCAGTTCCGCG	CGCGGAACTGATGAGATGAAGCTC
	2286	GACAACTCCACTGCTCCAATCGCA	TGCGATTGGAGCAGTGGAGTTGTC
	2287	GGCCAAGGATGGACCTTACGATGG	CCATCGTAAGGTCCATCCTTGGCC
	2288	GGTTCCGGAATTTGTCACCGCTTC	GAAGCGGTGACAAATTCGCGAACC
	2289	GCGCTGGATAGTCTGCGAGAAGCC	GGCTTCTCGCAGACTATCCAGCGC
40	2290	TGAGTCCAGTGCTGCCACCATGAA	TTCATGGTGGCAGCACTGGACTCA
	2291	TTGAATTGGGTGTCGGAGCGTTCT	AGAACGCTCCGACACCCAATTCAA
	2292	CGGCGGGCAGACAATGCTTTGAAC	GTTCAAAGCATTGTCTGCCCGCCG

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2293	GGGTCTGTCAAAGAGGGTGTCTGG	CCAGACACCCTCTTTGACAGACCC
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2295	ATCGAATTCGAGGAGGTCTCCAT	ATGGAGACCTCCTCGGAATTCGAT
2296	TCCGACCCTCAGAGTCGACTCATT	AATGAGTCGACTCTGAGGGTCGGA
2297	ATCAACGGCCACCTCCTCGCCGAG	CTCGGCGAGGAGGTGGCCGTTGAT
2298	AGCCACGGAATAATTCCGTCCACC	GGTGGACGGAATTATTCCGTGGCT
2299	GATCGCTTGCGTATCGAAAGACT	AGTCTTTGCGATACGCAAGCGATC
2300	TCCACGCCTTACCATCAACTGCAA	TTGCAGTTGATGGTAAGGCGTGGA
2301	GCCAAGCGATAGGCCAGAACTCAG	CTGAGTTCTGGCCTATCGCTTGGC
2302	AGCGTGTGGGTCAATTTAGCACGA	TCGTGCTAAAATGACCCACACGCT
2303	GTTATGCGCGGCTTACGAGTTCGA	TCGAACTCGTAAGCCGCGCATAAC
2304	TCTGTCCACGTAAC TTGCCTGCAG	CTGCAGGCAAGTTACGTGGACAGA
2305	TCGGCAGCCAATGATCATACCTCT	AGAGGTATGATCATTGGCTGCCGA
2306	TAAGCCCGATCCGGTCCTGTGTTT	AAACACAGGACCGGATCGGGCTTA
2307	ACATGGCAGACTAACAGGCCTCGC	GCGAGGCCTGTTAGTCTGCCATGT
2308	CATGGCTGCACTCTAAGTCGAACG	CGTTCGACTTAGAGTGCAGCCATG
2309	TCTTCAACCCACGCGGAACGATTG	CAATCGTTCGCGGTGGGTGAAGA
2310	CTCGTGTCTCCAGAGGATTGTCCC	GGGACAATCCTCTGGAGACACGAG
2311	TGAAGGCATCAACCCAGAGGATTT	AAATCCTCTGGGTGATGCCTTCA
2312	ACAGCTCGAAGGCAGCCACATTGG	CCAATGTGGCTGCCTTCGAGCTGT
2313	ACAACGAGTACCGCGACAGAAGGG	CCCTTCTGTGCGGTA CTGTTGT
2314	ATAACCGAAAAACCAGCCTGCGAT	ATCGCAGGCTGGTTTTTCGGTTAT
2315	ACAACTCAGCACTTTCGACGTCCA	TGGACGTCGAAAGTGCTGAGTTGT
2316	CGGGTTACTGGGTATCACCAATGC	GCATTGGTGATACCCAGTAACCCG
2317	CATCGGTTATCGCTGCACGCGCGT	ACGCGCGTGCAGCGATAACCGATG
2318	GAAGGAATCCCGGATAGTCCGTGG	CCACGGACTATCCGGGATTCCTTC
2319	GCATGGTCTCAGCCAAAGAACCTG	CAGGTTCTTTGGCTGAGACCATGC
2320	AGCCTGCGACGTTTCCCGACAGAC	GTCTGTGCGGAAACGTGCGAGGCT
2321	AAGAAAGGCGCACGGGATCGATAT	ATATCGATCCCGTGCGCCTTTCTT
2322	TGTCGCGAAGCCAAC TTTCAGTAA	T TACTGAAAGTTGGCTTCGCGACA
2323	GCGGCATGCAAGGTAGGTCTGGAT	ATCCAGACCTACCTTG CATGCCGC
2324	GGTGGCCATCTCCTCGAATTGCAT	ATGCAATTCGAGGAGATGGCCACC
2325	GCGTGCATAAGTTGCACATTGTGC	GCACAATGTGCAACTTATGCACGC
2326	TTGAGGTAGCGTTTTTCGCGCATAT	ATATGCGCGAAAACGCTACCTCAA
2327	ATCCCACTTGTGAGAGGGCGCATT	AATGCGCCCTCTCACAAGTGGGAT
2328	CGGTCAGCGAGCAGACATCAACCT	AGGTTGATGTCTGCTCGCTGACCG
2329	GCGTATCTTCGGGTGCAACACTTG	CAAGTGTTGACCCGAAGATACGC
2330	ATGCCATTGAACTCGCACTTTGCG	CGCAAAGTGCGAGTTCAATGGCAT
2331	CGATTCCCATCATAATGTGGGTCC	GGACCCACATTATGATGGGAATCG
2332	CAATTTGGATAATCCAGCCACGCC	GGCGTGGCTGGATTATCCAAATTG
2333	CGGCTTACCCTATGATTCCGTGCA	TGCACGGAATCATAGGGTAAGCCG



	2334	GGTGGACCATGCGCTGTGGTATGA	TCATACCACAGCGCATGGTCCACC
	2335	TATTTGTCGAAGATCGCAAGCGCC	GGCGCTTGCGATCTTCGACAAATA
	2336	GTCAGTGGGTTTTGAGAGCCCGCA	TGCGGGCTCTCAAACCCACTGAC
5	2337	AGGGGGTCGGGAAATCTGACAAAA	TTTTGTCAGATTTCCCGACCCCT
	2338	TGCTTGCTATCCGAAAAAGCAGG	CCTGCTTTTTTCGGATAGCAAGCA
	2339	TTATCGGATCAAATTCGGCTTCGG	CCGAAGCCGAATTTGATCCGATAA
	2340	TGCAGCAACGAGTTACCCGGACTT	AAGTCCGGGTAACTCGTTGCTGCA
	2341	TATACATGTCCGGAGGGGCACCCA	TGGGTGCCCCTCCGGACATGTATA
10	2342	TGCAAAACCGGAGGATGAACCCTT	AAGGGTTCATCCTCCGTTTTGCA
	2343	TCGGTCTAATGTCCACGCAGACAC	GTGTCTGCGTGGACATTAGACCGA
	2344	ATGTGTTTGCCACGCGCTCCTATT	AATAGGAGCGCGTGGCAAACACAT
	2345	TGGCGAGGCACGGCTCTAATTCGG	CCGAATTAGAGCCGTGCCTCGCCA
	2346	GCGACGACCCGAGCGACTTTTACA	TGTAAGAGTCGCTCGGGTCGTCGC
	2347	CTCAGAGAGTCTATCCGGCGCCCT	AGGGCGCCGGATAGACTCTCTGAG
15	2348	GGAACATCTCCTGGGTCCCTCAGA	TCTGAGGGACCCAGGAGATGTTCC
	2349	GCAACGCAGGGAAGTACTTAGCGA	TCGCTAAGTACTTCCCTGCGTTGC
	2350	TGACTTGGGCGGACAAAGAAACGC	GCGTTTCTTTGTCCGCCCAAGTCA
	2351	AGATCATCGGGACGCTTCATGCTA	TAGCATGAAGCGTCCCGATGATCT
	2352	CCCTTCTGACCGCTAAGGCCATAA	TTATGGCCTTAGCGGTCAGAAGGG
20	2353	CGTGAGCCGTGGGGTGTCTCTGTA	TACAGAGACACCCACGGCTCACG
	2354	TACCTTGGTCTGCTCCGCTTTTGT	ACAAAAGCGGAGACGACCAAGGTA
	2355	TCGCCGCAAAATGCTACGTGAAAA	TTTTCACGTAGCATTTTGCGGCGA
	2356	GAGTGACCTAATGGCTGCCCGACT	AGTCGGGCAGCCATTAGGTCACTC
	2357	AAAGGAACTTGGCCAACCCATATGG	CCATAGGGTTGGCCAAGTTCCTTT
25	2358	TGTTTTCGCACTCCACCTAATCGC	GCGATTAGGTGGAGTGCGAAAACA
	2359	CAATGGGTTTCATAAGGGCAGGCA	TGCCTGCCCTTATGAAACCCATTG
	2360	GCCTAACACACAAGGGTCCCTCTG	CAGAGGGACCCTTGTGTGTTAGGC
	2361	CGTCATGCGGTCCGAGGATCGATC	GATCGATCCTCGGACCGCATGACG
	2362	CCACACGGGCACGGAGTAATATCT	AGATATTACTCCGTGCCCGTGTGG
30	2363	CATCAGACATAGGTGCGGTGCCGA	TCGGCACGCGACCTATGTCTGATG
	2364	AGATGAAACCAAGGGAGGACGCAG	CTGCGTCTCCTCCCTGGTTTCATCT
	2365	GGCTACCCATAGGCTCAGCAGCAC	GTGCTGCTGAGCCTATGGGTAGCC
	2366	GGCTTGTGAGGGTGTGTTCTCGAC	GTCGAGAACACACCCTCACAAAGCC
	2367	TGTGTTACGGCGAATGCAACAGTC	GACTGTTGCATTGCGCGTAACACA
35	2368	CGATAACAGGTGCGCGCGTTACTA	TAGTAACGGCGCGACCTGTTATCG
	2369	TGATAAAGTGAGGCTCCAGCGCGA	TCGCGCTGGAGCCTCACTTTATCA
	2370	AATTGTGCACGGATCTGCACGGCG	CGCCGTGCAGATCCGTGCACAATT
	2371	GCAATGTACTGTCACCAAGTGCGCA	TCGCCACTGGTGACAGTACATTGC
	2372	GGCATATCGGTAACACTTGGTCGG	CCGACCAAGTGTTACCGATATGCC
40	2373	GGGTCTCAAACCAGCGTGGCCGCT	AGCGGCCACGCTGGTTTGAGACCC
	2374	GTCTCCGGGACCATTGAGCTGGAG	CTCCAGCTCAATGGTCCCGGAGAC

	2375	GGCCTTCGGCATTGAGACGGGTTG	CAACCCGTCTGAATGCCGAAGGCC
	2376	CGTGATAGGCCACAGCGCTCAATT	AATTGAGCGCTGTGGCCTATCACG
	2377	GGCAGGCCCGCGAGGATGATTAAC	GTTAATCATCCTCGCGGGCCTGCC
	2378	CGGGTATGGTTGATAACAGCGTGG	CCACGCTGTTATCAACCATAACCCG
5	2379	ACGACGTCCTTGGGACCGTATTGT	ACAATACGGTCCCAAGGACGTCGT
	2380	CTGATATCGAGCCTGAGCCTTTTCG	CGAAAGGCTCAGGCTCGATATCAG
	2381	TCCCATTGGCCTGTATGCTGGCCT	AGGCCAGCATACAGGCCAATGGGA
	2382	GTGTCGTCGATTGTTTCATCGACG	CGTCGATGAAACAATCGACGACAC
	2383	CGAAAGCCAGTAGCCGATTGCGTG	CACGCAATCGGCTACTGGCTTTTCG
10	2384	GGTTCGGCTTATTCCACTGCGACA	TGTCGCAGTGGAATAAGCCGAACC
	2385	AGCGAGGGCTAACTTTTAAACGCG	CGCGTTAAAAAGTTAGCCCTCGCT
	2386	CGGCGCTGATGACGGGACTCGATT	AATCGAGTCCCGTCATCAGCGCCG
	2387	TCACAGTGCTCGGCGTAAGGACTA	TAGTCCTTACGCCGAGCACTGTGA
	2388	CCCATTACGAGCACACACCATGGC	GCCATGGTGTGTGCTCGTAATGGG
15	2389	GGCCGCTAATCTTTACGCATCACG	CGTGATGCGTAAAGATTAGCGGCC
	2390	ACGGCTTCCTAGTGTCAGCCCTT	AAGGGCTGGACACTAGGAAGCCGT
	2391	CTGTCAGGTCCTACCCAATGGCTC	GAGCCATTGGGTAGGACCTGACAG
	2392	CACAGCCCATCCCACTGAAGTCTG	AGCAGTTCAGTGGGATGGGCTGTG
	2393	ACAAACGATACACGCAACGCTGTG	CACAGCGTTGCGTGTATCGTTTGT
20	2394	TGGCGGCCAGCTAGCAGGCGAAGT	ACTTCGCCTGCTAGCTGGCCGCCA
	2395	ATCTCGAAACGATGCGTGCCTAAA	TTTAGGCACGCATCGTTTCGAGAT
	2396	ATCTCGAGAACAGCGTGCGTGCGG	CCGCACGCACGCTGTTCTCGAGAT
	2397	GAAGAAATCCGCCGACATCTACGG	CCGTAGATGTGGCGGATTTCCTC
	2398	GCGGAGCAACCTTGGCTGTTTCTA	TAGAAACAGCCAAGGTTGCTCCGC
25	2399	CGCGTTCCGAAGACTTGTTGTTTG	CAAACAACAAGTCTTCGGAACGCG
	2400	TGACCTGAAGCCCATCCATAAGCA	TGCTTATGGATGGGCTTCAGGTCA
	2401	TGGTATTCATTCCGGATAAGCGGG	CCCGCTTATCCGGAATGAATACCA
	2402	GCGTTGCGGGTCATTGATGCAAAC	GTTTGCATCAATGACCCGCAACGC
	2403	ACCGCTTTCTGTGTAGAGCCCTGA	TCAGGGCTCTACACAGAAAGCGGT
30	2404	CAAATAGACAATCGCAGCTTCGGG	CCCGAAGCTGCGATTGTCTATTTG
	2405	TGTCCTGACAAATCAAGGTGCAGG	CCTGCACCTTGATTGTGTCAGGACA
	2406	AAATTGCACTCGCGGAGATTTCCT	AGGAAATCTCCGCGAGTGCAATTT
	2407	TGACGCCCATTCTATATGGTGCA	TGCACCATATAGAAATGGGCGTCA
	2408	TGTTCCGACAGGGCACTGCTAGAC	GTCTAGCAGTGCCCTGTCGGAACA
35	2409	TCGCTGGCTTGGGAAGGCCTTCGT	ACGAAGGCCTTCCCAAGCCAGCGA
	2410	GTGCACCTCCGTTGGCGTAGAATG	CATTCTACGCCAACGGAGGTGCAC
	2411	CTCATTGGGGACCGATCGGGTTGC	GCAACCCGATCGGTCCCAATGAG
	2412	GCCAGTGTCTGTCAATGGATGGGA	TCCCATCCATTGACAGACACTGGC
	2413	TTGCCCGGCAGGTTCTGTGTAATG	CATTACACAGAACCTGCCGGGCAA
40	2414	ACCCGCGAACCAGACGCACTTCT	AGAAGTGCGTCTCGGTTCCGCGGT
	2415	TCCGTGCGATTGGTCAAGGTTGAT	ATCAACCTTGACCAATCGCACGGA

	2416	AGGGCGTCTCGGTTGAACCTCGGT	ACCGAGGTTCAACCGAGACGCCCT
	2417	TGACCGTTCAAAGAGCAAGCCAAC	GTTGGCTTGCTCTTTGAACGGTCA
	2418	ACACTCACCTGCTGTCCCTGCTGA	TCAGCAGGGACAGCAGGTGAGTGT
5	2419	GCGTTTAACTCCTTGGGTGGTGGT	ACCACCACCCAAGGAGTTAAACGC
	2420	CGCCTGCGCAGGTAACCTCCGCA	TGCGGAGAGTTACCTGCGCAGGCCG
	2421	AATCGAATTTCCCAGCGGCTGTTT	AAACAGCCGCTGGGAAATTCGATT
	2422	AAGCAGGTGGGATCCTGGGGATCA	TGATCCCCAGGATCCCACCTGCTT
	2423	AATCCCAGACTCGCTCTTCGTGCT	AGCACGAAGAGCGAGTCTGGGATT
10	2424	ACGGTTATAAGGGCCGGCTGCGAC	GTCGCAGCCGGCCCTTATAACCGT
	2425	TACGAGAGCGGGCTTAGACGTCGC	GCGACGTCTAAGCCCGCTCTCGTA
	2426	GCGATTTTGACCCACGGTTATCGA	TCGATAACCGTGGGTCAAATCGC
	2427	AGCTGTATAATTTGGATGGCGCGA	TCGCGCCATCCAAATTATACAGCT
	2428	TCCGCGAGTCTTAGCCGATTGAAC	GTTCAATCGGCTAAGACTCGCGGA
15	2429	GGCATCAGCTCCGTAAGCCGATAG	CTATCGGCTTACGGAGCTGATGCC
	2430	TGTTATTGGCAGTTCGAGCGACAG	CTGTCGCTCGAACTGCCAATAACA
	2431	GCGAGCCTTTTTGCTTGGGAAGAG	CTCTTCCCAAGCAAAAAGGCTCGC
	2432	AGAAGAAAAGGTCAGCGTCGACGA	TCGTCGACGCTGACCTTTTCTTCT
	2433	CGGGTCGACCCTTGAAGCATAACC	GGTTATGCTTCAAGGGTCGACCCG
20	2434	CTCGGTTTTACAAACTTACCGCG	CGCGGTAAGTTTGTGAAAACCGAG
	2435	GCAGTCCTATCCGGAGCCTGACAA	TTGTCAGGCTCCGGATAGGACTGC
	2436	AAGGTGCGCTATTTGTTGTCGGTC	GACCGACAACAAATAGCGCACCTT
	2437	AGTGGAATCCATGCCGACACCTGA	TCAGGTGTCGGCATGGATTCCACT
	2438	TACAGGCGTAATTCTGCGAGGGA	TCCCTCGCAGGAATTACGCCTGTA
25	2439	CCGAAGTGCGAGAAGCACGTTGTT	AACAACGTGCTTCTCGCACTTCGG
	2440	AAGGACTGGTATGGCCGGAGCTTT	AAAGCTCCGGCCATACCAGTCCTT
	2441	GGACACCGCCAACCTCATAGTTGC	GCAACTATGAGGTTGGCGGTGTCC
	2442	AATGGTGTTGCGCTGGACTIONAC	GTGGTAGTCCAGGCGAACACCATT
	2443	TAGGAAAGCGTACACGGGAATCCG	CGGATTCCCGTGTACGCTTTCCTA
30	2444	TCTACCCCCAATGATGAGGACGTC	GACGTCTCATCATTGGGGTGAGA
	2445	CGTGTCCGTGTGACACTGTCCATG	CATGGACAGTGTACACGGACACG
	2446	TCCAGGCTGTTGCGGATACGGTAG	CTACCGTATCCGCAACAGCCTGGA
	2447	GTAGGCAAAATGGTCGCGATCAAT	ATTGATCGCGACCATTTGCCTAC
	2448	ATCTCCGTGGACCCGATTGTGACA	TGTCACAATCGGGTCCACGGAGAT
35	2449	GAATATGCCGTCAACGCTATGGGC	GCCCATAGCGTTGACGGCATATTC
	2450	TTCCGGAAGCGTTTGGTAACTTTG	CAAAGTTACCAAACGCTTCCGGAA
	2451	TTGATAGGAATACCAGGGCCTGG	CCAGGCCCTGGTATTCCTATCGAA
	2452	GGCCATTTGAGGAGGATTATGCAA	TTGCATAATCCTCCTCAAATGGCC
	2453	ACCTTCTGACCTGGACTTTTGGCG	CGCCAAAAGTCCAGGTCAGAAGGT
40	2454	GACCAATCCGCAGTTGAGCAACAG	CTGTTGCTCAACTGCGGATTGGTC
	2455	TCGGCCACTCACCATGAGTGTAGG	CCTACACTCATGGTGAGTGGCCGA
	2456	AGCGCTCACATGTTGAAAACGGG	CCCGTTTTCGAACATGTGAGCGCT

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2457	TAACGCAAAGGCGCGATCCTCGCT	AGCGAGGATCGCGCCTTTGCGTTA
2458	TGGGTGGGCCAAATATTACTGCAA	TTGCAGTAATATTTGGCCCACCCA
2459	GTCCTCGAAAGGGGCATCCAAACA	TGTTTGGATGCCCCCTTCGAGGAC
2460	CCCATCTGGTGGGAGGCGTTATCA	TGATAACGCCTCCCACCAGATGGG
2461	GTGCGCGGTCTGCAAACCTCGCCAT	ATGGCGAGTTTGCAGACCGCGCAC
2462	TGTGTTGCCAACCTAGGTCATCA	TGATGACCTAGGGTTGGCAACACA
2463	CTGATGCTGTTCTCGTCGGTTGAC	GTCAACCGACGAGAACAGCATCAG
2464	AAGCTGCAAAGGTGAGCGTGCCA	TGCCACGCTCACCTTTTGCAGCTT
2465	TCTGACGCGTGCTTGGGAGTCTAT	ATAGACTCCCAAGCACGCGTCAGA
2466	GAATTACTTGGAGGCGCCGTGCAA	TTGCACGGCGCCTCCAAGTAATTC
2467	GATTCTTCCCGACCTAGGTTGGCC	GGCCAACCTAGGTCGGGAAGAATC
2468	CGCAGCGTATCCCATGTTGCTTGA	TCAAGCAACATGGGATACGCTGCG
2469	GAGATGGAATTGTTGCCCAAAGA	TCTTTGGGCGAACAATTCCATCTC
2470	GATGCCTGGATCGGTCTAGCGTCA	TGACGCTAGACCGATCCAGGCATC
2471	GCAGCGACTGCTAAGCTATCTCGG	CCGAGATAGCTTAGCAGTCGCTGC
2472	AGGGCTAATTTACATCGCCTTGCC	GGCAAGGCGATGTAAATTAGCCCT
2473	AAGTGCACATCCTCACGAAGCGAT	ATCGCTTCGTGAGGATGTGCACTT
2474	TCAGGCAGCCGTAATTAATGCGC	GCGCATTTAATTACGGCTGCCTGA
2475	CCACTGGGGAAATCGCACTGTTGG	CCAACAGTGCGATTTCGCCAGTGG
2476	TTGTCCAAAGCCACCTACGACAGA	TCTGTCGTAGGTGGCTTTGGACAA
2477	TGGGCGGAATAGATTGGGTGTCTT	AAGACACCCAATCTATTCCGCCCA
2478	TAGAATTTCGCCTCTTCTAGCCGCC	GGCGGCTAGAAGAGGCGAATTCTA
2479	CATTACTTCCTGCAGATGCGATGC	GCATCGCATCTGCAGGAAGTAATG
2480	GGAAATGCTAGCTGGGGTAATCGC	GCGATTACCCCAGCTAGCATTTC
2481	GCCGCCACTTGCGAATCTACATCT	AGATGTAGATTGCGAAGTGCGGGC
2482	ACAATAGCGGACAGCTCGCCAGAT	ATCTGGCGAGCTGTCCGCTATTGT
2483	AGTTAGGCTCTCGGTGCGGTCCAT	ATGGACCGCACCGAGAGCCTAACT
2484	TGGGCCTGAGAAGCGGTTAATAGG	CCTATTAACCGCTTCTCAGGCCCA
2485	ACGCTCTGAGCGACGCCTATCGTA	TACGATAGGCGTCGCTCAGAGCGT
2486	CCTGGTGATCGTGTCACGACTCA	TGAGTCTGGGACACGATCACCAGG
2487	GCGTGTCATTGCTTGAGGTTTC	GAAACCTCAAGCGAATGGACACGC
2488	ATCCTGAACGGCGATGACCACCAC	GTGGTGGTCATCGCCGTTCAGGAT
2489	TTACGTTTCTACCGATCAACGCC	GGCGTTGATCGGTGAGAAACGTAA
2490	GCCGTCTTGAGTGGCTAAAAGGCA	TGCCTTTTAGCCACTCAAGACGGC
2491	ATCTACGATGCGGCTCGAAGTGTT	AACACTTCGAGCCGCATCGTAGAT
2492	AACCAAGACTCGTCCCCAAACGAA	TTCGTTTGGGGACGAGTCTTGTT
2493	AACTGCGGTGGTGGAGGCAGGTGC	GCACCTGCCTCCACCACCGCAGTT
2494	TGCGATCTTCTCCACCTACAGCGC	GCGCTGTAGGTGGAGAAGATCGCA
2495	AGGCGCTTAGAACCCTGAAGGCAG	CTGCCTTCACGGTTCTAAGCGCCT
2496	TGGAATAATTTGGGAAACGCTGGA	TCCAGCGTTTCCAAAATTTTCCA
2497	CCAGCGCCGCACCTTCTCCAATAG	CTATTGGAGAAGGTGCGGGCGCTGG

	2498	TAGACGGCTGGCGAATCTTACGGT	ACCGTAAGATTCGCCAGCCGTCTA
	2499	TACCATACAAGAGAACGAGCCGCA	TGCGGCTCGTTCTCTTGTATGGTA
	2500	GTAGCCGAGAGCAATTTTCACCGC	GCGGTGAAAATTGCTCTCGGCTAC
5	2501	GCAAACTCCCTGCCCTTTAGCCT	AGGCTAAAGGGCAGGGGAGTTTGC
	2502	ATCCCGCTGATAACCGCCAGGATA	TATCCTGGCGGTTATCAGCGGGAT
	2503	AGTCTCAGTTCGGCGCAACGGTAG	CTACCGTTGCGCCGAAGTGAAGT
	2504	AACCTACAGTCGCCGCAATGCATT	AATGCATTGCGGCGACTGTAGGTT
	2505	ATACACGTTTCAGCCGGAACAAT	ATTGTTGCCGGCTGAAACGTGTAT
	2506	ACGACGGGACGTGCCCTCGTTGAT	ATCAACGAGGGCACGTCCCGTCGT
10	2507	AAGTCCAAACTCGAATGGGGCAGT	ACTGCCCCATTGAGTTTGGACTT
	2508	GATTTATTGGCGCGGTAACGACCT	AGGTCGTTACCGCGCCAATAAATC
	2509	TGTTTTAGAGGCTACCCTGCCAT	ATGGCAGGGTAGCCTCTGAAAACA
	2510	ACGGTCTCAGGGAAATGCGATCTC	GAGATCGCATTTCCTGAGACCGT
15	2511	GACTTGAAACCGCCTATGCCACA	TGTGGGCATAGGCGGTTTCAAGTC
	2512	CGATCGGTTGTGTGCTGTCTTACC	GGTAAGACAGCACACAACCGATCG
	2513	AGTAGCACAATGCCTCATTTCCGC	GCGGAAATGAGGCATTGTGCTACT
	2514	CTCGCTATCTACGCGTCTCCGAAA	TTTCGGAGACGCGTAGATAGCGAG
	2515	AGCCCGTTACGGCATCTAGGATTC	GAATCCTAGATGCCGTACGGGCT
20	2516	TCGCGATGGCGAGAGTTCAGAATA	TATTCTGAACTCTCGCCATCGCGA
	2517	TTACAGGATTCCAAAACCCGCAA	TTTGCGGGTTTTTGAATCCTGTAA
	2518	CGGTACCAACGCGCGGGCATATGA	TCATATGCCCGCGCGTTGGTACCG
	2519	TGCCAGTATTATCCGTGCCAGCCG	CGGCTGGCACGGATAATACTGGCA
	2520	ATTCAGACCTCGGGACAACCTGG	CCAGGTTGTCCCGAGGTCTGAAAT
25	2521	GAAGTGCGCGTAACCTAGGGAGCC	GGCTCCCTAAGTTACGCGCACTTC
	2522	TTGGCCAGGTCATCACTCTGCCAT	ATGGCAGAGTGATGACCTGGCCAA
	2523	ATCGGCCCGTATTAGCTGCCCTCC	GGAGGGCAGCTAATACCGGCCGAT
	2524	CGCAGGTAAGGCCGAGCAATGTTT	AAACATTGCTCGGCCCTTACCTGCG
	2525	TTGGGAACGTGCTAGGCGGCCCTC	GAGGGCCGCTAGCACGTTCCCAA
30	2526	CATCTCGGCACACTGGTGCTGTAT	ATACAGCACCAGTGTCGCCGAGATG
	2527	ACGCGTAAATCAACGACGTGGTCG	CGACCACGTCGTTGATTACGCGT
	2528	CGTAGGTGGTAAATGTTGGCCCAG	CTGGGCCAACATTTACCACCTACG
	2529	TTCGAGCCAGAATAAACGGTTGG	CCAACCGTTTTATTCTGGCTCGAA
	2530	AGAGATATTCGGCCTCGGTGCGAGA	TCTCGACCGAGGCCGAATATCTCT
35	2531	CGACAAAGTTTCTCGCGAGCAACT	AGTTGCTCGCGAGAACTTTGTCG
	2532	ATTGCCGCGTCTCGTATCAAAAGA	TCTTTTGATACGAGACGCGGCAAT
	2533	CGGAGAATGGATGCAGGTTCTTCG	CGAAGAACCTGCATCCATTCTCCG
	2534	TATAATCATTTGCGACTCGCCCCA	TGGGGCGAGTCGCAAATGATTATA
	2535	AATTTTCCCGATTGGAAGAAGCG	CGCTTCTTCAAATCGGGGAAAATT
40	2536	TCGCATACTTCGTGCGCGAGTATT	AATACTCGCCGACGAAGTATGCGA
	2537	CGTGAGCCGTTCTCATCCAAGCGG	CCGCTTGGATGAGAACGGCTCACG
	2538	GCAGAATCGAATTGGGGTGGGTTT	AAACCCACCCCAATTGATTCTGC

	2539	CTCTCGGTTTCTCAACCGAGCTCG	CGAGCTCGGTTGAGAAACCGAGAG
	2540	GACCAGTTAGTGCAATGGTTGGCG	CGCCAACCATTGCACTAACTGGTC
	2541	TTCTCGCACAGCTAGTCAGCCGAT	ATCGGCTGACTAGCTGTGCGAGAA
5	2542	CCAAGTCTTGCGTGAGCGATCCTG	CAGGATCGCTCACGCAAGACTTGG
	2543	GCGAAAGTGGCTCGTATTTCTCCA	TGGAGAAATACGAGCCACTTTTCGC
	2544	CCTCGGGACTGTCCGACTGAAAAA	TTTTTCAGTCGGACAGTCCCAGAG
	2545	AGGCGAGTGTACGGCTCATCCATG	CATGGATGAGCCGTACACTCGCCT
	2546	GCGGCTCTGCCTACGATATTACACA	TGTGAATATCGTAGGCAGAGCCGC
10	2547	TGCACCTGTCTGTAGATTTGCGGT	ACCGCAAATCTACAGACAGGTGCA
	2548	CATAAAGCACGGACGCGACTTGAT	ATCAAGTCGCGTCCGTGCTTTATG
	2549	CCCTCAACGTAGGGCGTGACTTTC	GAAAGTCACGCCCTACGTTGAGGG
	2550	GGGTCATCGTGCA GTTATGCCGTA	TACGGCATAACTGCACGATGACCC
	2551	CCCGGATAATCCTTTGTCCAGCCG	CGGCTGGACAAAGGATTATCCGGG
15	2552	TCCGATAAGCGAACTCACATGGGT	ACCCATGTGAGTTCGCTTATCGGA
	2553	CCTGCTGGTTCGGTCGTAAGCGAA	TTCGCTTACGACCGAACCAGCAGG
	2554	GAGGCACCAATCGGTCTGAAAATG	CATTTTCAGACCGATTGGTGCCTC
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	2558	CCCGCTTATCTGTACTCGATCGCA	TGCGATCGAGTACAGATAAGCGGG
	2559	TTTTGGGGATCCCTATTAGGCGCA	TGCGCCTAATAGGGATCCCCAAAA
	2560	AGTGACAGCGCTCACCACGGTCCC	GGGACCGTGGTGAGCGCTGTCACT
	2561	CCATGAGTGTTTCGGGACATCGTA	TACGATGTCCCGAAACACTCATGG
25	2562	GCCACATTCTGCTACCTCCGTGTT	AACACGGAGGTAGCAGAATGTGGC
	2563	TCCTGTGCTTTGTGACGTGCTAGG	CCTAGCACGTACAAAAGCACAGGA
	2564	GACCGCATATACACCTGATGGGCC	GGCCCATCAGGTGTATATGCGGTC
	2565	GTAGGCCCGTCGTTAACCATCTCA	TGAGATGGTTAACGACGGGCCTAC
	2566	CGGCTCGCGAAATGGAGTTTAGCG	CGCTAAACTCCATTTGCGGAGCCG
30	2567	GCTGATCGGCTTTTCACCGCTATA	TATAGCGGTGAAAAGCCGATCAGC
	2568	TATCAAATCGTTGGCAGCGGACTA	TAGTCGCGTGCCAACGATTTGATA
	2569	TTGGCGAGGATCCCTAGGCGTACT	AGTACGCCTAGGGATCCTCGCCAA
	2570	AAGTCCTGAGGCCGTTTCGTTTCT	AGAAACCGAACGGCCTCAGGACTT
	2571	ACTCCGGACATCTCGGCCAGAGAT	ATCTCTGGCCGAGATGTCCGGAGT
	2572	CCAAGGGGAACACAGGATCGTAGA	TCTACGATCCTGTGTTCCCTTGG
35	2573	GTGGCCTAAATCCGCCTTCTCAAC	GTTGAGAAGGCGGATTTAGGCCAC
	2574	CACTCCGTCTCGTCCATTAAATGCG	CGCATTAAATGGACGAGACGGAGTG
	2575	TCAAGAACCAGTGCCGGTCAGCA	TGCTGACCGGCACTGGGTTCTTGA
	2576	GAATCAATTTTCCAGGGACGGGAC	GTCCCGTCCCTGGAAAATTGATTC
40	2577	ATCGGTGTGCTGGAGCGCCAGAGT	ACTCTGGCGCTCCAGCACACCGAT
	2578	GCCTCTCCTATGACGATGACCCAC	GTGGGTATCGTCATAGGAGAGGC
	2579	TGGGCGCGCTTTTAAGACTACATC	GATGTAGTCTTAAAAGCGCGCCCA

	2580	CGTTGGGTACCGTTCTATCAACCG	CGGTTGATAGAACGGTACCCAACG
	2581	GCAGTGAGCTGGGTTCAATGCTTC	GAAGCATTGAACCCAGCTCACTGC
	2582	CATCATCCACACAGGCAGGTGTGT	ACACACCTGCCTGTGTGGATGATG
	2583	AGACAAAGGTCCCCATTGCGAAAT	ATTTGCAATGGGGACCTTTGTCT
5	2584	ATACTCGTCGACGAGAAGCGGAAA	TTTCCGCTTCTCGTCGACGAGTAT
	2585	GCAGAATGTGTTGTCTTCGCAGCC	GGCTGCGAAGACAACACATTCTGC
	2586	CACCATGCCTTCATCTTGGCCTAG	CTAGGCCAAGATGAAGGCATGGTG
	2587	ACTCTTCAACGCCAGGTTAAGCCA	TGGCTTAACCTGGCGTTGAAGAGT
	2588	GCGACCTGCGGCGTGTGTATTCTC	GAGAATACACACGCCGCAGGTGCG
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	2590	ACCGTCGAATCTTGCGGCCAATGT	ACATTGGCCGCAAGATTGACCGGT
	2591	TAATGCATGCTCCCGGCTCACGTT	AACGTGAGCCGGGAGCATGCATTA
	2592	TCTGTACACACCACGTCGTGCACA	TGTGCACGACGTGGTGTGTACAGA
	2593	CATGGGGTTGTCAGACGACACCTA	TAGGTGTCGTCTGACAACCCCATG
15	2594	AATCTGATGCTCGCTGTAGGACGG	CCGTCCTACAGCGAGCATCAGATT
	2595	TCGAAACCGCGGAAAGGGTAAAA	TTTTACCCTTTCCCGCGGTTTCGA
	2596	TGGGGGACGGGCGTCTAATCCTCC	GGAGGATTAGACGCCCGTCCCCCA
	2597	AGGCATGCACCCATGCTGCCAGAG	CTCTGGCAGCATGGGTGCATGCCT
	2598	TCCCAATGGCCTGTCAAGCATAAA	TTTATGCTTGACAGGCCATTGGGA
20	2599	GAACCTGAGCCTTTGCTAGCACGA	TCGTGCTAGCAAAGGCTCAGGTTT
	2600	CGAATTGATAGCGTTACGGGCGAA	TTCGCCCGTAACGCTATCAATTG
	2601	TTGCACGCGCGCGAACGACTATTC	GAATAGTCGTTGCGCGCGTGCAA
	2602	TGCGGTGAAGCAGTCCAAGGTCAG	CTGACCTTGGAAGTCTTACCGCA
	2603	TGAGGACCATCCAATGGATCGGTT	AACCGATCCATTGGATGGTCCTCA
25	2604	TCGGTGATTGGTAATTTGGATCCG	CGGATCCAAATTACCAATCACCGA
	2605	GCGGGCAGGTAGTTTGACTGGATG	CATCCAGTCAAACCTACCTGCCCGC
	2606	CAAGCACAAGCCCATGAAATTTCA	TGAAATTTGATGGGCTTGTGCTTG
	2607	CGGTACAGCGGATAGCCAAGGATA	TATCCTTGGCTATCCGCTGTACCG
	2608	CCATGCTCTTCGCTGCAGCATACT	AGTATGCTGCAGCGAAGAGCATGG
30	2609	CGCGGCAAAGATTAATTCGCGCG	CGCCGGGAATTAATCTTTGCCGCG
	2610	GAAGACCCGTCGGGTTTCCATAC	GTATGGAAACCCGACGGGTCTTC
	2611	CTGGCAAGGAGGATGTGGCTCGTG	CACGAGCCACATCCTCCTTGCCAG
	2612	CTGTGCAGGGGGTGGCTCTGTTGA	TCAACAGAGCCACCCCTGCACAG
	2613	TTCAATAATGATCACGAGGCCCA	TGGGGCCTCGTGATCATTATTGAA
35	2614	TGGTGATGCGAAGCCTTACCTTTG	CAAAGGTAAGGCTTCGCATACCA
	2615	CTGCCACCATCTACGGCGCAGTCT	AGACTGCGCCGTAGATGGTGGCAG
	2616	TTTGCCAGCTCTCGCAGAAGTTA	TAACCTCTGCGAGAGCTGGGCAAA
	2617	AATTCAGACGCCACATCGACGGTC	GACCGTCGATGTGGCGTCTGAATT
	2618	CCGTGGTCTGCCTCGATTACCTAC	GTAGGTAATCGAGGCAGACCACGG
40	2619	GGCGAGGAATTTGGAACCTTATG	CATAAGGTTCCGAAATTCCTCGCC
	2620	ATCCGATGATCAGATACCGGCTGG	CCAGCCGGTATCTGATCATCGGAT

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2621	CCATAGACTAGCGCCAGAGTGCCC	GGGCACTCTGGCGCTAGTCTATGG
2622	TGTGGACCTAGAAAATTGCCAGCC	GGCTGGCAATTTTCTAGGTCCACA
2623	GAATAATCATCGCGGTCCTCATGG	CCATGAGGACCGCGATGATTATTC
2624	GGGATTGGCTCTTGGTTGGAAGAA	TTCTTCCAACCAAGAGCCAATCCC
2625	ATTGTGCTTCCTCGAACTGGGAAA	TTTCCCAGTTCGAGGAAGCACAAAT
2626	TGCCCCACCCCGTAAGTCAATAAT	ATTATTGACTTACGGGGTGGGGCA
2627	TCAGGACCGACGGTGCACCTAGTG	CACTAAGTGCACCGTCGGTCCTGA
2628	CCAGCCGTACAGTGCAATTTCCG	CGGAAATTGCACTGTGACGGCTGG
2629	CTTAAAGAGGCGCGAAGCACACA	TGTTGTGCTTCGCGCCTCTTTAAG
2630	TACCGCTCGTCGCGATCACAATGA	TCATTGTGATCGCGACGAGCGGTA
2631	CCGAGTGCGCGAAGTGTCTATGTG	CACATAGACACTTCGCGCACTCGG
2632	GCACCACTGCCCCGATCAAAACGTA	TACGTTTTGATCGGGCACTGGTGC
2633	TGCAGGCTTCTCAACGGCTGGGAG	CTCCAGCCGTTGAGAAGCCTGCA
2634	CTCCGTACGTATCCCGCGTGATAC	GTATCACGCGGGATACGTACGGAG
2635	GGAAGTGCAACTTAAAGCCCCGCC	GGCGGGGCTTTAAGTTGCACTTCC
2636	CGAACCGGCAGTCGATCGTTGCAT	ATGCAACGATCGACTGCCGGTTCG
2637	CCGTTAGTGGTCGACAGTTCGGTT	AACCGAACTGTCGACCACTAACGG
2638	TCAGGCTACGCCCTCAGCACTACA	TGTAGTGCTGAGGGCGTAGCCTGA
2639	TATACGGGCCGAGGTCCGTATTCTG	CGAATACGGACCTCGGCCCGTATA
2640	CCAACGTGTGACGAAGGGCCATTG	CAATGGCCCTTCGTACACGTTGG
2641	CTGCTCAGCGGTGCTTGAAAGACA	TGTCTTTCAAGCACCGCTGAGCAG
2642	GGAGATTGACTTCGCGTTTCACCA	TGGTGAAACGCGAAGTCAATCTCC
2643	ATGGTTCAGAAGGTTTCGTGCGGTT	AACCCGACGAACCTTCTGAACCAT
2644	GAGTGGAGCATTCTCGGCCCTCAA	TTGAGGGCCGAGAATGCTCCACTC
2645	TGGATTGGAACCAATCCCGCACAA	TTGTGCGGGATTGGTTCCAATCCA
2646	TGCTCTTGTTGGTCACTCGAGAGGA	TCCTCTCGAGTGACCACAAGAGCA
2647	TTGGGAGCACGGTTACCGCCTGTG	CACAGGCGGTAACCGTGCTCCCAA
2648	CAACGCGAGCTAACGGTAGTTTCG	CGAACTACCGTTAGCTCGCGTTG
2649	AACGCTGAGCGCTCACCTTCACCT	AGGTGAAGGTGAGCGCTCAGCGTT
2650	CCGTCGTAGATCTGGAGGCTTCAA	TTGAAGCCTCCAGATCTACGACGG
2651	GGATGGCATGGGCACACTGTAACC	GGTTACAGTGTGCCCATGCCATCC
2652	TCGCTCGTAGATATCCTTCACGCC	GGCGTGAAGGATATCTACGAGCGA
2653	GGAGCAATACCGCGTCCAAAACAC	GTGTTTTGGACGCGGTATTGCTCC
2654	TTGTTTCAGACTTAGGCGCTGCCCCA	TGGGCAGCGCCTAAGTCTGAACAA
2655	CGGCGGTACTCTTTCCACTGTCCT	AGGACAGTGGAAGAGTACCGCCG
2656	AAGACGATTGCCACGTGCCAGAG	CTCTGGCACGTGGGCAATCGTCTT
2657	AGGTGAGCGCAGGCATATTGCAGT	ACTGCAATATGCCTGCGCTCACCT
2658	CTCGGGCCTGTACAGCAAAGCCGT	ACGGCTTTGCTGTACAGGCCCGAG
2659	TGCGCGCTAGTGCTGCCTATGATC	GATCATAGGCAGCACTAGCGCGCA
2660	CCATCCTTTGCCTTGAGGGTAAGG	CCTTACCCTCAAGGCAAAGGATGG
2661	AACAACAGCGTAAGACGGACAGGG	CCCTGTCCGTCTTACGCTGTTGTT



	2662	GAGGCGGTCTGAGGCTCACAATATT	AATATTGTGAGCCTCGACCGCCTC
	2663	CGAGGTTAGACGCCTATGACCCAC	GTGGGTCATAGGCGTCTAACCTCG
	2664	AACTTGCTATACCGGGCGCAGCAA	TTGCTGCGCCCGGTATAGCAAGTT
5	2665	CGCGGTGAATCGCATACACAGCGC	GCGCTGTGTATGCGATTACCGCG
	2666	CACCGAATCAAGCCATATGGCTCT	AGAGCCATATGGCTTGATTCCGTG
	2667	TTCACAGCTATCCTAGGCGCTGCC	GGCAGCGCCTAGGATAGCTGTGAA
	2668	AGAAGCGCGAAGTGACCCCGCAT	ATGCGGGGTACACTTCGCGCTTCT
	2669	TGCATGGTATTTGCGTGCGATAGG	CCTATCGCACGCAAATACCATGCA
10	2670	GGCCGGACCTATGTGAGATGGAAA	TTTCCATCTCACATAGGTCCGGCC
	2671	TCAACCTGAGTCCTGATCCCAAGC	GCTTGGGATCAGGACTCAGGTTGA
	2672	TGCTTACCGTTCAGGGAGGCGTGT	ACACGCCTCCCTGAACGGTAAGCA
	2673	GGAGAGTTACGCGATGAGCCACCT	AGGTGGCTCATCGCGTAACTCTCC
	2674	CGGTATGCGGTGTACAGCTTTCGT	ACGAAAGCTGTACACCGCATACCG
	2675	GTAAGCCGGGTCTCGTGTGCGCGT	ACGGCGACACGAGACCCGGCTTAC
15	2676	GCGTAGTGCGAACGCCCGACCTA	TAGGTGCGGGCGTTCGCACTACGC
	2677	TCCTCGCGGCTTACGTCAAATTCG	CGAATTTGACGTAAGCCGCGAGGA
	2678	CGACGTTCAAAGCGGGAGAGGAGG	CCTCCTCTCCCGCTTTGAACGTCG
	2679	CGAGGCACCCGACATGTTGAGAT	ATCTCAACATGTCGGGGTGCCTCG
	2680	CTATTTCTGCGCCGCTCGGACAAG	CTTGTCCGACGCGGCACGAAATAG
20	2681	GGCTGCTCAGTGACGTGTCAACTG	CAGTTGACACGTCACTGAGCAGCC
	2682	ATCACTCGTGCGTACCCGACCGTC	GACGGTCGGGTACGCACGAGTGAT
	2683	CGAGATGTCCTATACCGTGGCGAA	TTCGCCACGGTATAGGACATCTCG
	2684	TCACACCGAGCCCCATAAATGAAA	TTTCATTTATGGGGCTCGGTGTGA
	2685	AGCTACGTGTCTCGAGCAAAAGCG	CGCTTTTGCTCGAGACACGTAGCT
25	2686	TCAGGGCGAGTTTTTTCAGCGGCG	CGCCGCTGAAAAAACTCGCCCTGA
	2687	TTCTGTTCTGTCTATTTTTGCCCG	CGGGGCAAAAATAGACAGAACGAA
	2688	TGGTATGCCCAGGATCCAGCCTAC	GTAGGCTGGATCCTGGGCATACCA
	2689	TCTCAGTCGTTAGGCCAATGGCGG	CCGCCATTGGCCTAACGACTGAGA
	2690	AAAGATCACCGTGGAGCGATCGGC	GCCGATCGCTCCACGGTGATCTTT
30	2691	TAGCAGGACTTGCACTCGTGATGC	GCATCACGAGTGCAAGTCCTGCTA
	2692	TGCCCACGGTACCGTTCAAGGCTG	CAGCCTTGAACGGTACCGTGGGCA
	2693	TGAGGTGCGTCGCCCTAAGTAATG	CATTACTTAGGGCGACGCACCTCA
	2694	AGCAAGGGTTACAACCCGCAACCC	GGGTTGCGGGTTGTAACCCTTGCT
	2695	CACAACAGCCAGTATTCGCCACAA	TTGTGGCGAATACTGGCTGTTGTG
35	2696	GGCAACACCATACTCGACGAGCTC	GAGCTCGTCGAGTATGGTGTGTC
	2697	GGCTGGATTGACAATTTAGCCCT	AGGGGCTAAATTGTCAATCCAGCC
	2698	CGTGAGAAATGCTACACGCGTCAG	CTGACGCGTGTAGCATTCTCAGC
	2699	CGCATCTGCCCATTTTGTTCCTT	AAGGAACAAAATGGGGCAGATGCG
	2700	GTCGGCCTAGTCGGCAGAACGGTG	CACCGTTCTGCCGACTAGGCCGAC
40	2701	TCCCTCACCTTCCAAAAATGTGCT	AGCACATTTTGGGAAGGTGAGGGA
	2702	GGGCAAGAACATGAGAACAGACCG	CGGTCTGTTCTCATGTTCTTGCCC

	2703	TCGTCCTGGTACGACTTGCGTAGA	TCTACGCAAGTCGTACCAGGACGA
	2704	TGGCGGTTGCATGTGATGATCAAG	CTTGATCATCACATGCAACCGCCA
	2705	CCTCGCGTGAGTAAAAACCGTCCG	CGGACGGTTTTTACTCACGCGAGG
	2706	ACTTCCGCCACAGAATGCGGCCAG	CTGGCCGCATTCTGTGGCGGAAGT
5	2707	GTGTAGAGCTTGGGTAGCCCCGTT	AACGGGGCTACCCAAGCTCTACAC
	2708	CGCAGCATCCGAGTTAACACACAT	ATGTGTGTAACTCGGATGCTGCG
	2709	ATGAGCCTGGGATGATCCGCTGGT	ACCAGCGGATCATCCAGGCTCAT
	2710	CCTGGCATAAGTGCCGACATGCTT	AAGCATGTCCGCACTTATGCCAGG
	2711	GCGCATGAAAACTACGACGGACG	CGTCCGTCGTAGTTTTTCATGCGC
10	2712	AAAGATGGGTCGATGGGAGCGTCT	AGACGCTCCCATCGACCCATCTTT
	2713	ATCCTGGGCACGAGCGGATTTATC	GATAAATCCGCTCGTGCCGAGGAT
	2714	TCACCGCATTTGATAGTTACGCGA	TCGCGTAACTATCAAATGCGGTGA
	2715	TGGTGGAGCGGACTCTGGTGTTAT	ATAACACCAGAGTCCGCTCCACCA
	2716	CACAATGAAAAACAATGGCCCCA	TGGGGCCATTGTTTTTCATTGTG
15	2717	CCTTGCCGCGCTTGTTGGTACCAAC	GTTGGTACCACAAGCGCGGCAAGG
	2718	CCGAGACCTTTGCCACACGAAAGA	TCTTTCGTGTGGCAAAGGTCTCGG
	2719	ACCGCGGTGTACACCTGAGCAGGC	GCCTGCTCAGGTGTACACCGCGGT
	2720	GTCGTACGCTTACCGCAGCGGAGA	TCTCCGCTGCGGTAAGCGTACGAC
	2721	TCGTAATTTGACCGACACACGCAG	CTGCGTGTGTGGTCAAATTACGA
20	2722	CCTAGACGGATACCCTGAGCGGAA	TTCCGCTCAGGGTATCCGTCTAGG
	2723	AAGCGACAGCAGAGGTTCAAGTCGC	GCGACTGAACCTCTGCTGTGCTT
	2724	GCGTGACGATATCACCTGGGCGT	ACGCCCAGGTGATATCGTCCACGC
	2725	GTCGGAGAGCCAGTGGTACGGCTT	AAGCCGTACCACTGGCTCTCCGAC
	2726	TATCCGCACGGTATAGCAGTTGCA	TGCAACTGCTATACCGTGCGGATA
25	2727	CATCAGTCGGGCTACCTTCAGCCT	AGGCTGAAGGTAGCCCGACTGATG
	2728	CGGATTAATGCCTTTCCTCGGAAT	ATTCCGAGGAAAGGCATTAATCCG
	2729	TTCGTGTCGCCAAGCTAATGCAAG	CTTGCAATTAGCTTGGCACGACGAA
	2730	GGCCGAGACCACCAGTAACAGGTT	AACCTGTTACTGGTGGTCTCGGCC
	2731	CGCGCGGAAGCATTGAAGTTACTA	TAGTAACTTCAATGCTTCCGCGCG
30	2732	TCGGCTTACCGCTTCGTCTGACTT	AAGTCAGACGAAGCGGTAAGCCGA
	2733	GACTGACGTCAAGGCAAGCAACAC	GTGTTGCTTGCCTTGACGTCAGTC
	2734	AGAGGAAGGAGGGGCTGTGACAGA	TCTGTACAGCCCCCTCCTTCCTCT
	2735	TTCCAATGCGAGAGATGGCAGGCT	AGCCTGCCATCTCTCGCATTGGAA
	2736	AAATGGGGTGCTTCGAATATGTCG	CGACATATTCGAAGCACCCCATTT
35	2737	GCTGTCGGATTATTGCACGCCTGT	ACAGGCGTGCAATAATCCGACAGC
	2738	CCGACTTTGTTTATGTTGCTGGCG	CGCCAGCAACATAAACAAAGTCGG
	2739	GCTGCGATATAACCCGTCCAGAA	TTCTGGGACGGGTTATATCGCAGC
	2740	TGAGCTGGGCGTCAACTCCGAAGA	TCTTCGGAGTTGACGCCAGCTCA
	2741	CCCAAGCATCCTAAATCTCCCTCG	CGAGGGAGATTTAGGATGCTTGGG
40	2742	CGACAGCAATCCACATGCATTCTT	AAGAATGCATGTGGATTGCTGTGCG
	2743	TGAATGGTTCGGAAACCAATGCAT	ATGCATTGGTTTCCCAGCATTCA

	2744	CTTTGCATCGAGATGCGGGGTAGC	GCTACCCCGCATCTCGATGCAAAG
	2745	TCCATTTCTCCGCAACTCTCAGG	CCTGAGAGTTGCGGAGGAAATGGA
	2746	CCACTACGCCATCCTGACAACGAG	CTCGTTGTCAGGATGGCGTAGTGG
	2747	TAGTAAGGCCAATGTACGCCGTCC	GGACGGCGTACATTGGCCTTACTA
5	2748	GTCATGCATATGGGGCCTGTTTTC	GAAAACAGGCCCCATATGCATGAC
	2749	ACCGGTAGACGTTAGCGGGTTCAA	TTGAACCCGCTAACGTCTACCGGT
	2750	TTGGTTCAAACGGCCACACGTCTC	GAGACGTGTGGCCGTTTGAACCAA
	2751	GACACAACTGCAAGGGAGGCATG	CATGCCTCCCTTGCAGTTTGTGTC
	2752	CTCGAGCGCTGTCATCATATCGGC	GCCGATATGATGACAGCGCTCGAG
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	2754	ACAGCCTAAATGGCGCAAGACCGA	TCGGTCTTGCGCCATTTAGGCTGT
	2755	CCGATGATGTAAGCCGTCGGCCCT	AGGGCCGACGGCTTACATCATCGG
	2756	AGGAGCAAACAAACGCCAGTGACA	TGTCACTGGCGTTTGTTCGTCCT
	2757	ACGAATTGGGTAGCCGGAAGTGA	TCTCAGTCCGGCTACCCAATTCGT
15	2758	CTGTTCCAGTTCGGCAAGTGCGGC	GCCGCACTTGCCGAAGTGAACAG
	2759	AGACAAGTCAGGAACGCGTTCCG	CGGAAACGCGTTCCTGACTTGTCT
	2760	AGACGACGGCCAGATACGCTGCCA	TGGCAGCGTATCTGGCCGTCGTCT
	2761	AGGAAGCGCTTCTCCGGTTCTTC	GAAGAACCGGAAGAAGCGCTTCCT
	2762	GATGGACGCAAACACAAGGCGATC	GATCGCCTTGTGTTTGCCTCCATC
20	2763	CGCATAGCAGTCTCCGCATCTTGG	CCAAGATGCGGAGACTGCTATGCG
	2764	TGGTTCGGGTGTGCAACAGATAAA	TTTATCTGTTGCACACCGGAACCA
	2765	CCGTATGCCACCTCCAGAAGTCAA	TTGAGTTCTGGAGGTGGCATAACG
	2766	GTAAAGGAACCCCTCGGGAATCCT	AGGATTCCCGAGGGGTTTCTTTAC
	2767	GCCTGATGCTCGTTAAATTCGCT	ACGCAATTTTAACGAGCATCAGGC
25	2768	TCGCACTTGACCATGAGATCTGA	TCAGATCTCATGGTCCAAGTGCGA
	2769	TTCTCAGGCTGGGCAAGAGTCTGT	ACAGACTCTTGCCAGCCTGAGAA
	2770	CGGACCTGGGGATGCTGGGATTAC	GTAATCCAGCATCCCCAGGTCCG
	2771	TCGAGCCGATAGGGTTGGCATTGC	GCAATGCCAACCCTATCGGCTCGA
	2772	TACGTGTGTCCACACACGTCGTA	TACGACGTGTGTGGGACACACGTA
30	2773	TGTGAAATTCGCGTTTCGCATCTT	AAGATGCGAAACGCGAATTTACA
	2774	TTGCAATGCTCCAAAAAACTGCC	GGCAGTTTTTTTGGAGCATTGCAA
	2775	TCTCATCATGGCTGTGGCTTTGAC	GTCAAAGCCACAGCCATGATGAGA
	2776	ATTACACCGCTTGGTTTGGAGTGG	CCACTCCAAACCAAGCGGTGTAAT
	2777	GCCGTGCAATGCACAGAGTTCAAG	CTTGAAGTCTGTGCATTGCACGGC
35	2778	GAGATCAGACCGTGTGCGATGCTG	CAGCATCCGACACGGTCTGATCTC
	2779	CCACCTATCTTGATGCGACCTGGA	TCCAGGTCGCATCAAGATAGGTGG
	2780	CCGATCGCCGTTTATGTCTACGGC	GCCGTAGACATAAACGGCGATCGG
	2781	GAAAATCACGGTAAGGCACGTTCC	CGAACGTGCCTTACCGTGATTTTC
	2782	GATTCTCGCTTCCCAACGAGCATA	TATGCTCGTTGGGAAGCGAGAATC
40	2783	TGTGAAATGTGGCAGTCTCAGGGA	TCCCTGAGACTGCCACATTTACA
	2784	CGATCCTGCGTGCCTCATCCAGGC	GCCTGGATGAGGCACGCAGGATCG

	2785	CCCTCAAGTGGGCGAGGGTTTTCA	TGAAAACCCCTCGCCCACTTGAGGG
	2786	TCGCCTCCGCCTCGTGTGTAGAAG	CTTCTACACACGAGGCGGAGGCCA
	2787	TTCGCTTTCAGCTCATTGGAACGA	TCGTTCCAATGAGCTGAAAGCGAA
	2788	TGTAATCTGAACAAGCGGACCCCT	AGGGGTCCGCTTGTTTCAGATTACA
5	2789	TGGAATCTTTCTTGAGCGCCGTGA	TCACGGCGCTCAAGAAAGATTCCA
	2790	GGCTTTCATCTTTAACCGCTCGGT	ACCGAGCGGTTAAAGATGAAAGCC
	2791	TGATCCGAGCCATTCCTAATCACC	GGTGATTAGGAATGGCTCGGATCA
	2792	TGGTAGGCGTGATGTCCTACGCAA	TTGCGTAGGACATCACGCCTACCA
	2793	AGGCATCGGTAAGAAGGCCCTATG	CATAGGGCCTTCTTACCGATGCCT
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	2795	ACATGGACGAAATTACGCCCCTCA	TGACGGGCGTAATTTTCGTCCATGT
	2796	ACAGAAAGGTGGGGAGCCTAGCGT	ACGCTAGGCTCCCCACCTTTCTGT
	2797	AGGCTTGCGAACATGGGTAGTGAC	GTCACTACCCATGTTTCGCAAGCCT
	2798	GCGTGGGCCTTGCTCCTGTTAAC	GTTAAACAGGAGCAAGGCCACGC
15	2799	GAATACAGAGCGTCCGATGTGCCC	GGGCACATCGGACGCTCTGTATTC
	2800	GCGACTCTGTAGGGAGCGCGATAT	ATATCGCGCTCCCTACAGAGTCGC
	2801	GGTGCATCATATGCGTCGCATCG	CGATGCGACGCATATGAGTGCACC
	2802	CTGTCCCACGGGGAAACCTTACTT	AAGTAAGGTTTCCCCGTGGGACAG
	2803	TGGCTTACTGTGCGCAATCTAGGCC	GGCCTAGATTGCGACAGTAAGCCA
20	2804	GCACTCAGTTTCCGGTATCCCATG	CATGGGATACCGGAAACTGAGTGC
	2805	GTGAGGTTACGTAAGGCACAGCG	CGCTGTGCCTTACGTGAACCTCAC
	2806	GTAACGCCTTTGTCCCCAGCGTAT	ATACGCTGGGGACAAAGGCGTTAC
	2807	GCATTGATATGGTCGGTCTCGCCT	AGGCGAGACCGACCATATCAATGC
	2808	GTGGGTTTAAGTGACAACGGACGC	GCGTCCGTTGTCACTTAAACCCAC
25	2809	CAAACCCCTGCCGAAGATGTTGGT	ACCAACATCTTCGGCAGGGTTTTG
	2810	TCCGAGGAGACTGAACCTGCTACC	GGTAGCAGGTTCAGTCTCCTCGGA
	2811	CGGGGAAGAACGGATTGCTAAAT	ATTTAGCGAATCCGTTCTTCCCCG
	2812	TGGTTAGCTTATGTCCGAGCCACC	GGTGGCTCCGACATAAGCTAACCA
	2813	ACGCGTCGATGAACCTAAGGCTCGC	GCGAGCCTTAGTTCATCGACGCGT
30	2814	TTCTCCTGACGAGTACGCACTGGG	CCCACTGCGTACTCGTCAGGAGAA
	2815	TCCGCGGTTGCCGGTTTGTAGGA	TCCTAACAAACCGGCAACCGCGGA
	2816	TGGCGCATCTTTCAGGGGATGATG	CATCATCCCCTGAAAGATGCGCCA
	2817	TCTTTGGTCCTTGGTGTTTACGCG	CGCGTAAACACCAAGGACCAAAGA
	2818	GAGAACTCCCGCTACAAAGGAGCC	GGCTCCTTTGTAGCGGGAGTTCTC
35	2819	TTAACGTGGGAACCGTTGGTGAAT	ATTCACCAACGGTTCCACGTTAA
	2820	GGGACACCATCCTTGGGTTTGTTA	TAACAAACCCAAGGATGGTGTCCC
	2821	CAACAAACCGCCTTGGGAAGTGAC	GTCACCTCCAAGGCGGTTTGTG
	2822	TTGAAGGCCACCGATACTGATCGC	GCGATCAGTATCGGTGGCCTTCAA
	2823	TCGTAATAGAACTGCGCCCAATGC	GCATTGGGCGCAGTTCTATTACGA
40	2824	GGCACGTTGCCAAGTTGGATCCA	TGGATCCAACCTTGGGCAACGTGCC
	2825	ACATAGCTTGGCCGGACACCCACC	GGTGGGTGTCCGGCCAAGCTATGT

	2826	CTTGCCGCCTTGCGAGTGGCTAAA	TTTAGCCACTCGCAAGGCGGCAAG
	2827	AATGGCTCGCCAGATACCGCAGCC	GGCTGCGGTATCTGGCGAGCCATT
	2828	CAAAAGGCGTGTCGAACTTTTCA	TGAAAAGTTCGGACACGCCTTTTG
	2829	CGTCCACTTAGGTGGAGATACGCC	GGCGTATCTCCACCTAAGTGGACG
5	2830	GAGCCTCTTCGTCCTGAAGACCGA	TCGGTCTTCAGGACGAAGAGGCTC
	2831	AACATCAAGCGGCAATCTCCCTTC	GAAGGGAGATTGCCGCTTGATGTT
	2832	CGTCCTGACATTATTAGCGCGTGC	GCACGCGCTAATAATGTCAGGACG
	2833	TGTGCAGACCCTAACGACCTACGG	CCGTAGGTCGTTAGGGTCTGCACA
	2834	TTAGGTGCGCCTAGACCCTCCGTA	TACGGAGGGTCTAGGCCGACCTAA
10	2835	TCACATCGCTTAACTGAGCGCATT	AATGCGCTCAGTTAAGCGATGTGA
	2836	AGACCTTCCCACGCGAGATGCTAC	GTAGCATCTCGCGTGGGAAGGTCT
	2837	TTCTTGCCAAAATGTGTCCAACCA	TGGTTGGACACATTTTGGCAAGAA
	2838	CAGTTTTTCATTGCAGCGAAAGCAA	TTGCTTTCGCTGCAATGAAACTG
	2839	GTGCCGATCCCGAGACAAGTTCCG	CGGAACCTTGCTCGGGATCGGCAC
15	2840	CATCCGGCCTCAGTGATTCTTACC	GGTAAGAATCACTGAGGCCGGATG
	2841	TGCTGGAAGCCACAAACGTTACGT	ACGTAACGTTTGTGGCTTCAGCA
	2842	GAACGGCCAGGGGACAACATATCGT	ACGATAGTTGTCCCCTGGCCGTTT
	2843	TCATCTAGGTCGAAGCGCAAGACA	TGTCTTGCGCTTCGACCTAGATGA
	2844	TTTGGTTACCAGCACCCATGTTCC	GGAACATGGGTGCTGGTAACCAAA
20	2845	GACAACAGTCTGTCCGCCACATCC	GGATGTGGCGGACAGACTGTTGTC
	2846	GCCAACAGGAGATGCTTGACCAT	ATGGTGCAAGCATCTCCTGTTGGC
	2847	CTAAGGACGCATTGACCCCTGAAC	GTTCAGGGGTCAATGCGTCCTTAG
	2848	GGTCGCGTAGTGAGTCAGAGGCGT	ACGCCTCTGACTCACTACGCGACC
	2849	TTACCTCATGAACCTTCGCGGCG	CGCCGCGAAGGGTTCATGAGGTAA
25	2850	TATACAGCATCGTCGCCGGGCATA	TATGCCCCGGCGACGATGCTGTATA
	2851	GCTTAGTGGCGTCTTCGTCGTAGG	CCTACGACGAAGACGCCACTAAGC
	2852	TGCACTCCGCAACCTTGTAATC	GATTTACAAGGTTGCGGAGTGCA
	2853	AACCCGTCATGCCGACTCCATCTA	TAGATGGAGTCGGCATGACGGGTT
	2854	AGCACTAGTGGCGTGCGACTTTGC	GCAAAGTCGCACGCCACTAGTGCT
30	2855	TAAAAAGTGCCGCTAACCACGGAG	CTCCGTGGTTAGCGGCACTTTTTA
	2856	CGCGGAATATTTGTGTCGCGATT	GAATCGGACGACAAATATTCCGCG
	2857	TTCTGCTATGCGTATGGGGGCCCG	CGGGCCCCCATACGCATAGCAGAA
	2858	CGAACTACTGCGTCAGCCTCTCCC	GGGAGAGGCTGACGCAGTAGTTCG
	2859	AGATGACGAATTAGCGGGGTTGGG	CCCAACCCCGCTAATTCGTCATCT
35	2860	AATAACAGTGGCAATGAGCGGGAA	TTCCCGCTCATTGCCACTGTTATT
	2861	ATATGTTGATTCCCGTGCTGCACA	TGTGCAGCACGGGAATCAACATAT
	2862	AGAGTGGGCACCACCAGGCAGACA	TGCTGCTGGTGGTGGCCACTCT
	2863	AGGCCTGGGTTTCTGCGTCTTAGT	ACTAAGACGCAGAAACCCAGGCCT
	2864	CGGACGTGACAAACGGACATACCC	GGGTATGTCCGTTTGTACGTCGG
40	2865	CAAGTGTTTCGGCCCCAACTCTCGA	TCGAGAGTTGGGCCGAAACACTTG
	2866	GAACCCTTATCGGGATAGGCCCAA	TTGGGCCTATCCCATAAGGGTTC

	2867	CAGGACGATACCAAGCAGAACGCC	GGCGTTCTGCTTGGTATCGTCCTG
	2868	GCGTCTTGTTGATTCTGCCCTAACC	GGTTAGGGCAGAATCACAAGACGC
	2869	AAACAACCATCAATGTCGGGTCCA	TGGACCCGACATTGATGGTTGTTT
5	2870	TGTAAGACCAGTTGGCGGCTCTC	GAGAGCCGCCAACTGGTCTTTACA
	2871	GCGTTTTGACTCGGTGGTCAGTCC	GGACTGACCACCGAGTCAAAACGC
	2872	TGTATGGAGGCACGGCAAAGTCTT	AAGACTTTGCCGTGCCTCCATACA
	2873	TTACCTAGGTTCCCGCTGACACGC	GCGTGTGAGCGGGAACCTAGGTAA
	2874	CGGCTCGTGGGAATCCTCTGAAGA	TCTTCAGAGGATTCCACGAGCCG
10	2875	CCGGCTCGGGCATTCTTGACCT	AGGTCCAAGAAATGCCCCGAGCCGG
	2876	CAACGATGGAATTGTCTCCTTGGG	CCCAAGGAGACAATTCCATCGTTG
	2877	CGGGCTATTATCGGGATTATGGGG	CCCCATAATCCCGATAATAGCCCCG
	2878	ACGTACCTGAAGATGCAACGGCGG	CCGCCGTTGCATCTTCAGGTACGT
	2879	CATGGTGCAGCACGCACAAGTAAC	GTTACTTGTGCGTGCTGCACCATG
15	2880	CGTCGATATGTCGGGCTATTGCCT	AGGCAATAGCCCGACATATCGACG
	2881	AAATGCAGGGTTAAGAGGAGGCC	GGGCCTCCTCTTAACCCTGCATTT
	2882	TGCAAGGACTGATTCTCCCGCTGT	ACAGCGGGAGAATCAGTCCTTGCA
	2883	GTTTTCGGAACGCCGAGAGTTCA	TGAACTCTGCGGCGTTCGAAAAC
	2884	CCCTCGATGGTTCATTGGGAAGAC	GTCTTCCCAATGAACCATCGAGGG
	2885	CCTGTTGCTCATAATGGTGGGGT	ACCCACCATATGAGCGAACAGG
20	2886	GAAAGAACGATCGCGGAATAGCTG	CAGCTATTCCGCGATCGTTCCTTC
	2887	TCCACCTGTGTGCCTTTATCCTCA	TGAGGATAAAGGCACACAGGTGGA
	2888	TCCTCCGTGAACCGCTGTAGCGCA	TGCGCTACAGCGGTTACGGAGGA
	2889	TTGAGATTTTACGGTTTCCCCGC	GCGGGGAAACCGTAAAAATCTCAA
	2890	CGATAGGACGTGGGCATGTCCCAG	CTGGGACATGCCACGTCCTATCG
25	2891	CCCGAACTTTGAGATCCGAGAACA	TGTTCTCGGATCTCAAAGTTCGGG
	2892	TCACGCAGCTAGAGTCGCGTTACC	GGTAACGCGACTCTAGCTGCGTGA
	2893	AGATAACGCCCACTGACGACATGC	GCATGTGTCAGTGGGCGTTATCT
	2894	ACGCTTAGAGCTCCGATGCCGAAT	ATTCGGCATCGGAGCTCTAAGCGT
	2895	GGGCGATAACTTAAATTGTGCCGC	GCGGCACAATTAAGTTATCGCCC
30	2896	AGGACGTTTCATGCGTCTCTTGCA	TGCAAAGAGACGCATGAACGTCCT
	2897	CGGCTGGTAGAACTGTGCATCGTA	TACGATGCACAGTTCTACCAGCCG
	2898	TTCGAAATGTACTTCCACGCGGA	TCCGCGTGGGAAGTACATTTGAA
	2899	GCAGGTTGGCTGTCTTGTGGAGTC	GACTCCACAAGACAGCCAACCTGC
	2900	CGTTTGGTTGCTTCAAGAACCGGT	ACCGGTTCTTGAAGCAACCAAACG
35	2901	CATACTTGGTTGTTGTGCCACGC	GCGTGGGCACAACAACCAAGTATG
	2902	GCGGTGCGCTGAAGTGTCTTATCC	GGATAAAACACTTCAGCCGACCCC
	2903	GTGACGGTTGATTAACGACCGTGG	CCACGGTCGTTAATCAACCGTCAC
	2904	CTTATGGCAGCGCCAGGGGCACTC	GAGTGCCCTGGCGTGCCATAAG
	2905	GTTAGGGGACCCACCTCGTTTGAT	ATCAAACGAGGTGGGTCCCCTAAC
40	2906	CAATATAAATGCCGCGCATCGAGT	ACTCGATGCGCGGCATTTATATTG
	2907	TTCTTCATCAGCAGTCCCCGAGAA	TTCTCGGGGACTGCTGATGAAGAA

	2908	AGTTGCGTCCCTTGATGGCATT	AAAATGCCATCAAGGGACGCAACT
	2909	CCGACTTTCGTCCACGATTCCTCT	AGAGGAATCGTGGACGAAAGTCGG
	2910	ACTTGCCGGACGACAGCAAAGAC	GTCTTTGCTGTCGTCCGGCCAAGT
5	2911	CACCGCGGTAGATGTATCCCTTCC	GGAAGGGATACATCTACCGCGGTG
	2912	GTTAGCTTTAGCTCGGCACGCCTG	CAGGCGTGCCGAGCTAAAGCTAAC
	2913	GCGCATAAGAAGGTCCGCTAAAGC	GCTTTAGCGGACCTTCTTATGCGC
	2914	ACATCATCACGCCTGGCGTGACCA	TGGTCACGCCAGGCGTGATGATGT
	2915	CCGGCGAAGTTTGGTGTGATTAGA	TCTAATCACACCAAACCTTCGCCGG
10	2916	TGCACCGCCAGATTGTGCTGAGTC	GACTCAGCACAATCTGGCGGTGCA
	2917	ACATGTGAAGTGAGTGCCGTCCAA	TTGGACGGCACTCACTTCACATGT
	2918	CCTCTGGAGGGGATTAGCCACGCT	AGCGTGGCTAATCCCCTCCAGAGG
	2919	CAATAGCCATGTCACTGGCAACGG	CCGTTGCCAGTGACATGGCTATTG
	2920	ACCCATGGTTCCAACGTTCTTTCG	CGAAAGAACGTTGGAACCATGGGT
15	2921	AATCTGGTCTTGGCATCCTCCAAA	TTTGGAGGATGCCAAGACCAGATT
	2922	GTATACCGGTGCATGCTGAAGCAA	TTGCTTCAGCATGCACCGGTATAC
	2923	AGTGTTCTGGTTCGAGTCGACCCG	CGGGTCGACTCGAACCAGAACT
	2924	CGGGTATTCGACACACAGAGGAC	GTCCTCGTGTGTGTCGAATACCCG
	2925	AGTGCAACAGAGCGCTTGGTCACG	CGTGACCAAGCGCTCTGTTGCACT
20	2926	TGCACCTATAGTTTGGTGCCGGTG	CACCGGCACCAAACCTATAGGTGCA
	2927	TGCTCACGTACCAGGACACTCGAG	CTCGAGTGTCCTGGTACGTGAGCA
	2928	AGTCCACACCTCGAACGACAGGCG	CGCCTGTCTGTCGAGGTGTGGACT
	2929	CGCCGACCTGGTCAAAGAGCGCTA	TAGCGCTCTTTGACCAGGTGCGCG
	2930	GCCTAAGGGCCTGTCGTTTTCCGA	TCGGAACGACAGGCCCTTAGGC
25	2931	TGTGCGTGCTTATGTTCCGGTCTC	GAGACCGGAACATAAGCACGCACA
	2932	CAACCGTTGGCCGTAACAAAATC	GATTTTGTACGGCCAACCGTTG
	2933	CGAGAATCAAGGCGTACCATCTCG	CGAGATGGTACGCCTTGATTCTCG
	2934	GCGTAGGCAGCCTCCAGGGAATGG	CCATTCCCTGGAGGCTGCCTACGC
	2935	GATGGTGTTTTCGCCAAGACCAAT	ATTGGTCTTGGCGAAAACACCATC
30	2936	CAAGCTAGGGACAGAATTGCCAC	GTGGGCAATTCTGTCCCTAGCTTG
	2937	TAAATAGGCGAAACCGTTCGTGGC	GCCACGAACGGTTTCGCCTATTTA
	2938	TCAAGACCCGCAATGTGTTTCATGT	ACATGAACACATTGCGGGTCTTGA
	2939	GCGGCTGGTAGACTCTTTGCACAA	TTGTGCAAAGAGTCTACCAGCCGC
	2940	CAGGCGTAAACCTGAACCAAACGG	CCGTTTGGTTCAGGTTTACGCCTG
35	2941	GCCGATCTGTGCTGAGGTTTCATCA	TGATGAACCTCAGCACAGATCGGC
	2942	GATATCGCGTCGCAATATCACGCG	CGCGTGATATTGCGACGCGATATC
	2943	CCCTGCACGATTAAGCCACCTGTA	TACAGGTGGCTTAATCGTGACGGG
	2944	TGACATACAGATTTGTGTGGCCCC	GGGGCCACACAAATCTGTATGTCA
	2945	GTTTGCGGCCGGTATTCACGATGT	ACATCGTGAATACCGGCCGCAAAC
40	2946	TTTTACCTGGCCATTGGTGAGCTC	GAGCTCACCAGTGGCCAGGTAAAA
	2947	CTCTACTCAATCAGGGTGGGAGCG	CGCTCCCACCCTGATTGAGTAGAG
	2948	GGGTTGGAGGGAGTCTTGACCATT	AATGGTCAAGACTCCCTCCAACCC

	2949	CGAGGTCGGTAAGGAAAAGCTTGC	GCAAGCTTTTCCTTACCGACCTCG
	2950	CTTTACGCAGGCACCTCCGAGCTG	CAGCTCGGAGGTGCCTGCGTAAAG
	2951	CATTGTATGGCCACGTGATTGACG	CGTCAATCACGTGGCCATACAATG
	2952	GTACGGTGCAGAGAGCGCCTAAGCG	CGCTTAGGCGCTCTCGCACCGTAC
5	2953	TTCCATATGCCGAAATGGACACAA	TTGTGTCCATTTGCGCATATGGAA
	2954	TACGCCTTCCGCTATAGCTCGTGA	TCACGAGCTATAGCGGAAGGCGTA
	2955	CTGTACGCCACGCATGAAGGGTGA	TCACCCTTCATGCGTGGCGTACAG
	2956	CTTACGCGTCCAATGACTGCCACC	GGTGGCAGTCATTGGACGCGTAAG
	2957	CACATGGTAGAACTCGATCGGCAG	CTGCCGATCGAGTTCTACCATGTG
10	2958	CGCACCGGAAACTAGTGGATGTGT	ACACATCCACTAGTTTCCGGTGCG
	2959	ACTATGGCAACCGACACTTGGTCC	GGACCAAGTGTCGGTTGCCATAGT
	2960	CTAGTTTGCGCTACCCACCTGCAA	TTGCAGGTGGGTAGCGCAAACCTAG
	2961	TAGTATCGCCCGACAATAGCCTGG	CCAGGCTATTGTCGGGCGATACTA
	2962	CCAATATTTACGGCCTGATCAGCG	CGCTGATCAGGCCGTAAATATTGG
15	2963	ATGGCTATCCCTTACTGGCTCGCC	GGCGAGCCAGTAAGGGATAGCCAT
	2964	CAAACTTGGCAGGCJTGGGACTT	AAGTCCCAAGCCTGCCAAGTTTTG
	2965	AATGACCGAGGCTGCAAGATTGAC	GTCAATCTTGCAGCCTCGGTCATT
	2966	ATCATCTTTGCGCCACCAGACATGG	CCATGTCTGGTGGCGAAAGATGAT
	2967	CGTTATTACCGATGCACACGTTGC	GCAACGTGTGCATCGGTAATAACG
20	2968	CACACTGGCAATCGCCTCCCTCGT	ACGAGGGAGGCGATTGCCAGTGTG
	2969	AGGTTGGTAGGAAATCGGAGCGCT	AGCGCTCCGATTTCTACCAACCT
	2970	GCTGAACCACTGTGGTCAAGATGC	GCATCTTGACCACAGTGGTTCAGC
	2971	CGTTGAGTACGACACGGTCGAGGT	ACCTCGACCGTGTCTGACTCAACG
	2972	TTTTTCCGCCGCAATGTGATCTAA	TTAGATCACATTGCGGCGGAAAAA
25	2973	ACAATACCTCGACCGCTCAGCATC	GATGCTGAGCGGTGCGAGGTATTGT
	2974	AGTATCCCTGCTGGCATAACGGG	CCCGTGTATGCCAGCAGGGATACT
	2975	TCTTGGGCTCGGTAGTTCAGCACT	AGTGCTGAACTACCGAGCCCAAGA
	2976	CCCTATATCGAGCCCATAGGGCGA	TCGCCCTATGGGCTCGATATAGGG
	2977	CACGAGTGGCATCAACGGCCTACT	AGTAGGCCGTTGATGCCACTCGTG
30	2978	TGCAGGGTCCGATGTGTTCAAGTA	TACTTGAACACATCGGACCCTGCA
	2979	GCTTGACCGCTGCTAACCTCGTAC	GTACGAGGTTAGCAGCGGTCAAGC
	2980	TTTTGCATCTCTCCACCATCCAGA	TCTGGATGGTGGAGAGATGCAAAA
	2981	AGAATGTGCACCGGCTTCCATCTT	AAGATGGAAGCCGGTGCACATTCT
	2982	TGTTATGACCCGCTCTGTGGCGTG	CACGCCACAGAGCGGGTCATAACA
35	2983	GGAGCTCCTGTTTCATCGAGGCTA	TAGCCTCGATGAAACAGGAGCTCC
	2984	CATTTTGCTGTTTGGGGTCCCAT	ATGGGACCCCCAAACAGCAAAATG
	2985	CCCGCTCCTTCACGTGAGACGAGA	TCTCGTCTCACGTGAAGGAGCGGG
	2986	GCGCTCAAGTCGATTGCCACAACC	GGTTGTGGCAATCGACTTGAGCGC
	2987	CGGTTGACGGAGACCGCAGTACTT	AAGTACTGCGGTCTCCGTCAACCG
40	2988	ACTCAAGACCGGTGCACCTCCAGC	GCTGGAGGTGCACCGGTCTTGAGT
	2989	TTTCGTGTGCATGCAAGTAATGGC	GCCATTACTTGCATGCACACGAAA



	2990	GCGGCGTTAGCTCGAGCTAACAAA	TTTGTTAGCTCGAGCTAACGCCGC
	2991	GGGTATCCTGCCCAGCAGTAATT	AATTACTGCTCGGGCAGGATACCC
	2992	GGCTCCGAATCTCTTGCCGGTCT	AGACCGGACAAGAGATTCCGAGCC
	2993	AGGATGGCCACGCCGAATCAAAGT	ACTTTGATTGCGCGTGGCCATCCT
5	2994	GTGCGGGGACGTTTACATAACGAG	CTCGTTATGTAAACGTCCCCGCAC
	2995	ACTTTTGACCTGAGGCCGCTTGCA	TGCAAGCGGCCTCAGGTCAAAAGT
	2996	ACTCCGCTTCAATGGAGACCGTTG	CAACGGTCTCCATTGAAGCGGAGT
	2997	GATCGGAATTGCGCGCCATATTGA	TCAATATGGCGGCGAATTCCGATC
	2998	ATGCGTGCCCATGGAATGACTTTT	AAAAGTCATTCCATGGGCACGCAT
10	2999	CCGCATCGCACGAAGGCAGGTCAT	ATGACCTGCCTTCGTGCGATGCGG
	3000	CACCCTATGCGTCTCCAATTCCTG	CAGGAATTGGAGACGCATAGGGTG
	3001	TGATATGCATCGCTGAGCCTCTGT	ACAGAGGCTCAGCGATGCATATCA
	3002	AGCTTCACACGCTCACTGAACCTG	CAGGTTCACTGAGCGTGTGAAGCT
	3003	AACCCGGAACCTCCTCTCACTCGG	CCGAGTGAGAGGAGGTTCCGGGTT
15	3004	CTCGTCAAAC TTGGCCGAGGAGTC	GACTCCTCGGCCAAGTTTGACGAG
	3005	GTAGCTGGCAACAGGCAATCAGGA	TCCTGATTGCCTGTTGCCAGCTAC
	3006	CTTGTCACGAATATTCGCCAAGCG	CGCTTGCGCAATATTCGTGACAAG
	3007	CAGTATCTGAAACACGGGGTGCTG	CAGCACCCCGTGTTTCAGATACTG
	3008	GGCTAAAATGGGCGCCACGTGTA	TACACGTGGGCGCCCATTTTAGCC
20	3009	ATGAGAGCCAAGCGCCTCAACTCC	GGAGTTGAGGCGCTTGCTCTCAT
	3010	TATTGTTAGGCACCGCTTCGCGCT	AGCGCGAAGCGGTGCCTAACAAATA
	3011	GGAAGTAGATTGCCAGTGCTCGCC	GGCGAGCACTGGCAATCTAGTTCC
	3012	AGTCGACCCCAAGGCAACTGGGTC	GACCCAGTTGCCTTGGGGTCGACT
	3013	GGTACTGTTAGCTCGACGATGGCC	GGCCATCGTCGAGCTAACAGTACC
25	3014	CCGCAATACTTGACGGTAACAGGG	CCCTGTTACCGTCAAGTATTGCGG
	3015	AATCCGGGTTTGAACGGTTGGAA	TTCCAACCGTTCAAACCCGGAATT
	3016	GACACGCAATCGGGTCTATGCGAA	TTGCGATAGACCCGATTGCGTGTC
	3017	GATTTTGGCGTCTCATTGCGTGAT	ATCACGCAATGAGACGCCAAAATC
	3018	TGCCATAGGGAGGAAACGCAATTA	TAATTGCGTTTCCTCCCTATGGCA
30	3019	GAGGTGCCCATGTTAGTGGTGTCC	GGACACCACTAACATGGGCACCTC
	3020	GCTTTAGCGGTCATACGACCACCA	TGGTGGTGTGATGACCGCTAAAGC
	3021	CCGCTACCAACAATCCGATTAACG	CGTTAATCGGATTGTTGGTAGCGG
	3022	GAGGATCTGGCCACATCGAGAAAG	CTTTCTCGATGTGGCCAGATCCTC
	3023	CTCGTTTGGTACCACGTTTGCCG	CGGCAAAACGTGGTACCAAACGAG
35	3024	AATACACGCGGCGTAAACAGACGA	TCGTCTGTTTACGCCGCGTGATT
	3025	TGTCATGGGCCAAATGACAGTGGC	GCCACTGTCATTTGGCCCATGACA
	3026	ACAGCACTTCCGACCCGTGTACGA	TCGTACACGGGTCGGAAGTGCTGT
	3027	CTCCGTAAAGAGCACAGCTTTGCC	GGCAAAGCTGTGCTCTTTACGGAG
	3028	ACGAACAGGTAGGGATCGGTCTC	GAGGACCGATCCCTACCTGTTCTG
40	3029	TGGATCCACCTTACCGCGCCATCG	CGATGGCGCGGTAAGGTGGATCCA
	3030	AGTATCAAATAGCGGCGCGGCAAG	CTTGCCGCGCCGCTATTTGATACT

3031	GAATTACATTGTGGATGGAGGCGG	CCGCCTCCATCCACAATGTAATTC
3032	CTCCTCGGGGAGTCGAGGAGTACG	CGTACTCCTCGACTCCCCGAGGAG
3033	AGTGTGAGCCAACTCCCACCAAT	ATTGGTGGGAGTTGGCTCGACACT
3034	AAATGACATCCGTTTGGCCACAGC	GCTGTGGCCAAACGGATGTCATTT
3035	CGAATCATATCGCCATCGAACTGG	CCAGTTCGATGGCGATATGATTCTG
3036	TATAATGCACTCGCTTGGTGCGCA	TGCGCACCAAGCGAGTGCATTATA
3037	GCCAAGCAGATGGTAATTATGGCG	CGCCATAATTACCATCTGCTTGGC
3038	CACGCGGGAAGAGCACGTAGAACT	AGTTCTACGTGCTCTTCCCGCGTG
3039	TACCCGAGAATTTGGAGAACAGCG	CGCTGTTCTCCAAATTCTCGGGTA
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3042	TACCCGCCACACATGAAAGTTGG	CCAACCTTCATGTGTGGGCGGGTA
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3045	TCTGACCGCAATAGGTGGTCATTG	CAATGACCACCTATTGCGGTCAGA
3046	ACTTTTGGCGGGCCCTCTCTCGT	ACGAGAGAGGGCCCGCCAAAAAGT
3047	CTGCCCAGATCATTGCGCGATCCG	CGGATCGCGCAATGATCTGGGCAG
3048	CGGAGGTTAAATGCTTTAACCGGC	GCCGGTTAAAGCATTTAACCTCCG
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3053	AGCTGTTAGGACCCGACAACCGGT	ACCGGTTGTGCGGTCTTAACAGCT
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3057	ACCTTTAACTTGTACCGCGGCC	GGGCCGCGGTACAAGTTTAAAGGT
3058	AGGGATGCAGAGGCACCACATGTT	AACATGTGGTGCCCTGTCATCCCT
3059	CGGTTGACGTATGAGCATCCGCA	TGCGGATGCTCATACGTGAACCG
3060	CAGGGCGATAGTCACATGGAGGTT	AACCTCCATGTGACTATCGCCCTG
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3062	CGAAGGGGTTGTGCAATTACCCGA	TCGGGTAATTGCACAACCCCTTCG
3063	AAAACGCACCGCAATGACAAAATT	AATTTTGTCAATTGCGGTGCGTTTT
3064	ATTCCTGGACAAGACCCTCAACCG	CGGTTGAGGGTCTTGTCAGGAAT
3065	CCTACCTGCCTGCTAGCGGTGAGG	CCTCACCGCTAGCAGGCAGGTAGG
3066	GCTCGTAAATGGGGAGGAATTGGA	TCCAATTCCTCCCCATTTACGAGC
3067	ACATGAAAACAGGCTCAATTGGGG	CCCCAATTGAGCCTGTTTTCATGT
3068	GTTCCGCACATGGATTGAGGTCTC	GAGACCTCAATCCATGTGCGGAAC
3069	GGCACCCAATACCACGAAGAAGAA	TTCTTCTTCGTGGTATTGGGTGCC
3070	AGGGGCATTTGAACTCCATCTTT	AAAGATGGAGTTCGAAATGCCCT
3071	CATCATCACAAGGAACGTGGTG	CACCGACGTTCTTTGTGATGATG

	3072	TAAAGACCCACCGTCAGCAGCAGC	GCTGCTGCTGACGGTGGGTCTTTA
	3073	CCCCAGGCGTAATGCACCACATAG	CTATGTGGTGCATTACGCCTGGGG
	3074	GCAGGTGGAACGCTAGTGGTTGAA	TTCAACCACTAGCGTTCGACCTGC
	3075	GGAACCTAGGAGTTCACGTCGCCA	TGGCGACGTGAACTCCTAAGTTCC
5	3076	GCAGATACGGCTAGCTGAGGTGGC	GCCACCTCAGCTAGCCGTATCTGC
	3077	CACAGGCCTAGAGCCTCGGCGTTC	GAACGCCGAGGCTCTAGGCCTGTG
	3078	GTTTTGCGCGCATGAGGTTCAATTA	TAATGAACCTCATGCGCGAAAAC
	3079	TTGCGCCTGATGCCAGCAGTACTA	TAGTACTGCTGGCATCAGGCGCAA
	3080	GATATCAGGCTTTCCCACTGCCGC	GCGGCAGTGGGAAAGCCTGATATC
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	3082	CATTGGTGTGGCTGAGAGTGGAC	GTCCACTCTCAGCCAACACCAATG
	3083	GTCGGCACTTGGGCACCATTAATA	TATTAATGGTGCCCAAGTGCCGAC
	3084	ATCGATCGGTGTCTCACCACGGAG	CTCCGTGGTGAGACACCGATCGAT
	3085	CGTAGCCTTCCACCGTGTGATAG	CTATCGACACGGTGGAAGGCTACG
15	3086	CGCTCTCCGTCTGAGGAAAAGGGG	CCCCTTTTCCTCAGACGGAGAGCG
	3087	TCGCCCCAGCCAAGGATATATTGC	GCAATATATCCTTGGCTGGGGCGA
	3088	TCTCTTGCAAGGAAGTCTGCCGTC	GACGGCAGAGTTCCTTGCAAGAGA
	3089	GTCCTGGACAGACGGAGGGGTGTTA	TAACACCCTCCGTCTGTCCAGGAC
	3090	GCCAAATTAAGCGGGCTCGTAATC	GATTACGAGCCCGCTTAATTTGGC
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	3092	TGGTCAAAAGAGCACGATCCAGGA	TCCTGGATCGTGCTCTTTTGACCA
	3093	CGCTACTAAGACGCCCTGTCCAC	GTGGACAGGGGCGTCTTAGTAGCG
	3094	CATACCTCCCGCTTGGATTCACTG	CAGTGAATCCAAGCGGGAGGTATG
	3095	CCGCGGAAGGAATGTCATCTACAA	TTGTAGATGACATTCTTCCGCGG
25	3096	CACGGGACATTCATTCACAGGACG	CGTCCTGTGAATGAATGTCCCGTG
	3097	AGGAGTCACCCACTCCGCACAAAA	TTTTGTGCGGAGTGGGTGACTCCT
	3098	TCATGACAGCGCACCCCATACCAT	ATGGTATGGGGTGGCTGTGATGA
	3099	GGTAGGGGACTATCGATCGTGCTG	CAGCACGATCGATAGTCCCCTACC
	3100	ATGTCTCACTACCGCACGTAGCGG	CCGCTACGTGCGGTAGTGAGACAT
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	3102	GAAGTCTGTGCGCCGGTGGACGGAC	GTCCGTCCACCGGCGACAGACTTC
	3103	CCGTAACGTGTATTTCGGACGAGCG	CGCTCGTCCGAATACACGTTACGG
	3104	CGTGGAAGCGACTTAACCAATCGT	ACGATTGGTTAAGTCGCTTCCACG
	3105	GGCATGGGCTATGCCTCACACTAG	CTAGTGTGAGGCATAGCCCATGCC
35	3106	GGGTGCTATTTAGCATCGTTCGT	ACGAACGATGCTGAAATACGACCC
	3107	AATGGTCGCGCAAACCGTAAGAAT	ATTCTTACGTTTTGCGCGACCATT
	3108	CTGGATTCCGTACGTCCAACGTTT	AAACGTTGGACGTACCGAATCCAG
	3109	CGCAAAAACACCCGTAGCCAAGAA	TTCTTGGCTACGGGTGTTTTGCG
	3110	TATGGATACGCTTTTGGACTGGGC	GCCCAGTCCAAAAGCGTATCCATA
40	3111	GCTTCAAACGCGCTTCACGCTGGT	ACCAGCGTGAAGCGCGTTTGAAGC
	3112	TACAGCCCGCTCTACCTCGCCACC	GGTGGCGAGGTAGAGCGGGCTGTA

	3113	TCAACCGATGTCAAAATGCACGTT	AACGTGCATTTTGACATCGGTTGA
	3114	AGCTCTCTCCGAAGTAGGGCGGTA	TACCGCCCTACTTCGGAGAGAGCT
	3115	ACGCACACATGGAGACTTGGCTCC	GGAGCCAAGTCTCCATGTGTGCGT
	3116	TTCTTGAAAGCTAGTGGGGCGCTA	TAGCGCCCCACTAGCTTTCAAGAA
5	3117	CAATCACGGCTGGGCTATTCTGTG	CACAGAATAGCCCAGCCGTGATTG
	3118	GTGGCGACCCGTCGGTGAAAGAGT	ACTCTTTCACCGACGGGTGCGCAC
	3119	CGTCGAATGCCGAACCAGTTAAGT	ACTTAACTGGTTCGGCATTGACG
	3120	TGCGTATTTGCATGCTCACAGCTG	CAGCTGTGAGCATGCAAATACGCA
	3121	CGCAGTTGGTTTGTGCACGGCTGC	GCAGCCGTGCACAAACCAACTGCG
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	3123	ACAGGTTCTCCACCACGATTTGA	TCAAATCGTGGTGGAGGAACCTGT
	3124	CTAGCGCGCTTTTAGGTCTTGCG	CGCAAGGACCTAAAAGCGCGCTAG
	3125	CAAAATCAAAGGGATCAACCGGTG	CACCGGTTGATCCCTTTGATTTTG
	3126	AACGTAACCCCACTGAGTCAGGCA	TGCCTGACTCACTGGGGTTACGTT
15	3127	TCAACCGGTGCACTTTAGAACGCC	GGCGTTCTAAAGTGCACCGGTTGA
	3128	ATCGCAAAGTTGCAGGCGAATACT	AGTATTCGCCTGCAACTTTGCGAT
	3129	ATATGTCCCTGGGTGCTGCACAAC	GTTGTGCAGCACCCAGGGACATAT
	3130	TGGCACTTTGTAGTGCTGCGGTGG	CCACCGCAGCACTACAAAGTGCCA
	3131	ACGCACGACGTCCTTCTAAGCTCG	CGAGCTTAGAAGGACGTCGTGCGT
20	3132	CCCACGTGCACTATAGGGATTTG	CGAAATCCCTATAGTGCACGTGGG
	3133	CCGCGCTTGGTCAGTCATCCTTGC	GCAAGGATGACTGACCAAGCGCGG
	3134	AGCGGCTCAGGGAATAACAACAGG	CCTGTTGTTATTCCCTGAGCCGCT
	3135	ACAACGCGATCGGAGGCAACCAGT	ACTGGTTGCCTCCGATCGCGTTGT
	3136	AGCAATTGCCTCCGTAGAAACCCA	TGGGTTTCTACGGAGGCAATTGCT
25	3137	GAGTCGTGGCATCGCCTGCTATCG	CGATAGCAGGCGATGCCACGACTC
	3138	TCTATGCAAATACTGCGCTTGCGA	TCGCAAGCGCAGTATTTGCATAGA
	3139	TCAGCTTAAGTTACGGTGTGGCCG	CGGCCACACCGTAACTTAAGCTGA
	3140	TCCAAGGTGCAACAGGGATCAGAA	TTCTGATCCCTGTTGACCTTGGA
	3141	GTTAGGCTGGCGTCAATAGCGCTT	AAGCGCTATTGACGCCAGCCTAAC
30	3142	GGTGTCTAAGGAAGAGGGCATCG	CGATGCCCTCTTCCTTATGACACC
	3143	CCGGCGGGCTAGATCAATATTTCT	AGAAATATTGATCTAGCCCCGCCG
	3144	CTAACGTCAAGTTTTACGCCCCGA	TCGGGGCGTAAACTTGACGTTAG
	3145	GCAGCACAGTTTTCCGATTTGCGG	CCGCAAATCGGAAACTGTGCTGC
	3146	CGCACGCAAGGGGAGGGATGACTG	CAGTCATCCCTCCCCTTGCGTGCG
35	3147	CGGGGCCGAAAAGGACGTCACAAG	CTTGTGACGTCCTTTTCGGCCCCG
	3148	TTCTCCAACACGGCTAACCGGTAG	CTACCGGTTAGCCGTGTTGGAGAA
	3149	TTACAGCCTGGCCGAGGTAGTTG	CAACTACCTCGGGCCAGGCTGTAA
	3150	TTTCGGGCAGCATGAGTTATCGAA	TTCGATAACTCATGCTGCCCGAAA
	3151	CTACTGGACGCCCTGCTTCGAAGT	ACTTCGAAGCAGGGCGTCCAGTAG
40	3152	GGTCGTCCGACGTGAAAAGACCAA	TTGGTCTTTTCACGTCGGACGACC
	3153	GTTTTGAGCTCTTTCTCCGCAGG	CCTGCGGAGAAAAGAGCTCGAAAAC

5	3154	GCGTGAAGGTACCCAGTGTCACAG	CTGTGACACTGGGTACCTTCACGC
	3155	TTTCTGAACGCTTCGACGCAACAC	GTGTTGCGTCGAAGCGTTCAGAAA
	3156	TGCTAATAAGCACGCCTAGCCCGT	ACGGGCTAGGCGTGCTTATTAGCA
	3157	AAATTAATTGTGGTGGCTCCGGCG	CGCCGGAGCCACCACAATTAATTT
	3158	TTACAATCCTCGGGCTCACTGACA	TGTCAGTGAGCCCGAGGATTGTAA
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	3160	GGGATAGGAGACCCTCGCAATGGT	ACCATTGCGAGGGTCTCCTATCCC
	3161	TTGCAGTACGTCCTTGCGCATGAA	TTCATGCGCAAGGACGTACTGCAA
	3162	TTGATCACTGGATTGGGTGCCAAC	GTTTCGCACCCAATCCAGTGATCAA
	3163	TCTGCAGACGTTGCGAGAGATGAT	ATCATCTCTCGCAACGTCTGCAGA
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	3165	GGGGTCCCGCAACAATAATGAAG	CTTCATTAGTTGTTGCGGGACCCC
	3166	CAACCTCTTATGTGGTGTGCGCGA	TCGCGCACACCACATAAGAGGTTG
	3167	CTCGCTGGGTTGCTGGAGTAGCAC	GTGCTACTCCAGCAACCCAGCGAG
	3168	CGTTGTATTGTGCAACGCGAAGTT	AACTTCGCGTTGCACAATACAACG
	3169	GGGCTCAAAGTGCCTGAGTCGAAA	TTTCGACTCAGGCACTTTGAGCCC
	3170	CTGCTGTGCCCTCTCAGTGAGAGC	GCTCTCACTGAGAGGGCACAGCAG
	3171	CGGACGTA CTGTTGCGAGTCCTCA	TGAGGACTCCGAACAGTACGTCCG
	3172	GTATACCACCATACCGGGACCGCA	TGCGGTCCCGGTATGGTGGTATAC

TABLE 3

Seq. ID No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
17	TTCGCCGTCGTGTAGGCTTTTCAA	TTGAAAAGCCTACACGACGGCGAA
18	GTTCCCAGTGAAGCTGCGATCTGG	CCAGATCGCAGCTTCACTGGGAAC
19	TACTTGGCATGGAATCCCTTACGC	GCGTAAGGGATTCCATGCCAAGTA
20	ACTAGCATATTTCAAGGGCACC GGC	GCCGGTGCCCTGAAATATGCTAGT
21	GAACGGTCAATGAACCCGCTGTGA	TCACAGCGGGTTCATTGACCGTTC
22	GCGGCCCTTGGTTCAATATGAATCG	CGATTCAATTGAACCAAGGCCGC
23	GATCGTTAGAGGGACCTTGCCCGA	TCGGGCAAGGTCCCTCTAACGATC
24	TGGACCTAGTCCGGCAGTGACGAA	TTCGTCACTGCCGACTAGGTCCA
25	ATAAACTACCCAGGACGGGCGGAA	TTCCGCCCGTCCTGGGTAGTTTAT
26	CATCGGTTGCGGCCAATCCAGATA	TATCTGGATTGGCGCGAACCGATG
27	GTCGGGCATAGAGCCGACCACCT	AGGGTGGTCGGCTCTATGCCCGAC
28	CTTGGGTCATGATTCACCGTGCTA	TAGCACGGTGAATCATGACCCAAG
29	TGCCTAACGTGCTAATCAGCAGCG	CGCTGCTGATTAGCACGTTAGGCA
30	CGCATGTTGGAGCATATGCCCTGA	TCAGGGCATATGCTCCAACATGCG
31	AGCCACTGCATCAGTGCTGTTCAA	TTGAACAGCACTGATGCAGTGGCT
32	GGTTGTTTTGAGGCGTCCCACACT	AGTGTGGGACGCCTCAAAACAACC
33	TCGACCAAGAGCAAGGGCGGACCA	TGGTCCGCCCTTGCTCTTGGTCGA
34	GACATCGCTATTGCGCATGGATCA	TGATCCATGCGCAATAGCGATGTC
35	GAAATACGAAGTCTGCGGGAGTCG	CGACTCCCGCAGACTTCGTATTTT
36	TGTCATGAATGATTGATCGCGCGA	TCGCGCGATCAATCATTCATGACA
37	ATATCGGGATTCTGTTCCCGGTGAA	TTCACCGGGAACGAATCCCGATAT
38	GCGAGCGTACCGAAGGGCCTAGAA	TTCTAGGCCCTTCGGTACGCTCGC
39	TTACCGGCAGCGGACTTCCGAATT	AATTCGGAAGTCCGCTGCCGGTAA
40	GTAATCGAGAGCTGCGCGCCGTCT	AGACGGCGCGCAGCTCTCGATTAC
41	CCTGTTAGCGTAGGCGAGTCGATC	GATCGACTCGCCTACGCTAACAGG
42	TAGCGGACCGGCAGAA TGAGTTCC	GGAATCATTCTGCCGGTCCGCTA
43	GGTACATGCACTACGCGCACTCGG	CCGAGTGC GCGTAGTGCATGTACC
44	AATTCATCTCGGACTCCCGCGGTA	TACCGCGGGAGTCCGAGATGAATT
45	GCCAAATCTGGATTGGCAGGAATG	CATTCCTGCCAATCCAGATTTGGC
46	TGCATTTTCGGTTGAGGCACATCC	GGATGTGCCTCAACCGAAAATGCA
47	CCGCTCAATTCACCATGCTTCGCT	AGCGAAGCATGGTGAATTGAGCGG
48	CTCGGAAAGGTGCAACTTTGGTGT	ACACCAAAGTTGCACCTTTCCGAG
49	AATTCGACCAGCAGAACGTCCCAT	ATGGGACGTTCTGCTGGTCAATT
50	GCCAGAGTCTCAACCTCACGGGAT	ATCCCGTGAGGTTGAGACTCTGGC
51	CCAACAAC TGGAACGGGAACCCGC	GCGGGTTCCCGTTCCAGTTGTTGG
52	GAGAACTGATCGCTGAGGGGCATG	CATGCCCTCAGCGATCAGTTCTC
53	GGCACACTAGACTTGTGGCACCGA	TCGGTGCCACAAGTCTAGTGTGCC

	54	TCACATCCAAATATGGTCCGCGAA	TTCGCGGACCATATTTGGATGTGA
	55	GTCTGCCGGTGTGACCGCTTCATT	AATGAAGCGGTCACACCGGCAGAC
	56	CATCGCAGAGCATAAACACCCTCA	TGAGGGTGTATTATGCTCTGCGATG
	57	GTTGGTATCTATGGCAGAGGCGGA	TCCGCCTCTGCCATAGATACCAAC
5	58	ACGAGGTGCCGCTGAGGTTCCATT	AATGGAACCTCAGCGGCACCTCGT
	59	GGAATGAGTGACCCAGGCACATT	AATGTGCCTGGGTCCACTCATTCC
	60	TGTCAATATGCGTCCGTGTCGTCT	AGACGACACGGACGCATATTGACA
	61	TGATGAGCCTCAGGGTACGAGGCA	TGCCTCGTACCCTGAGGCTCATCA
	62	CACCGCGGTGTTCCCTACAGAATGA	TCATTCTGTAGGAACACCGCGGTG
10	63	TTGTTGCCAATGGTGTCCGCTCGG	CCGAGCGGACACCATTGGCAACAA
	64	TTAACCTGCGTCTGCCCCCTTCCT	AGGAAAGGGGCAGACGCAGGTTAA
	65	AGGCGCGTTCCCTGCCTTAGTGACG	CGTCACTAAGGCAGGAACGCGCCT
	66	TAGGGCGATGGCACGAAGCTTCAA	TTGAAGCTTCGTGCCATCGCCCTA
	67	TGCATAGAGCCAAAGTCGGCGATG	CATCGCCGACTTTGGCTCTATGCA
15	68	TTGAGAGGCAGGTGGCCACACGGA	TCCGTGTGGCCACCTGCCTCTCAA
	69	TCCGCATTGTGAGAAAAACGAGC	GCTCGTTTTTCTCACAATGCGGA
	70	GGCGGTTTCCGTAGCTATAGGTGC	GCACCTATAGCTACGGAACCGCC
	71	GGTGAAAATTTCTAGCCACGGGC	GCCCGTGGCTACGAAATTTTACC
	72	CCGACGGAGGATGAAGACAATCAC	GTGATTGTCTTCATCCTCCGTCGG
20	73	CCAGTTTGCCCAATTCGCCAAAA	TTTTGGCGAATTGGGCCAACTGG
	74	GGATCTATTAGGCCGTGCGCACAG	CTGTGCGCACGGCCTAATAGATCC
	75	CGGATGTCACCGTTTGGACTTTCA	TGAAAGTCCAAACGGTGACATCCG
	76	ATCGCAAATCCTGCTCGTCCCTAA	TTAGGGACGAGCAGGATTTGCGAT
	77	CAGGGCATGCAATAATCGAGGTTT	GAACCTCGATTATTGCATGCCCTG
25	78	CATGCGTTGATATATGGGCCCAAG	CTTGGGCCCATATATCAACGCATG
	79	CAGCTGCAGCTTGTGACCAACCAC	GTGGTTGGTCACAAGCTGCAGCTG
	80	TTGTATGTCTGCCGACCGGCGACC	GGTCGCCGGTCGGCAGACATACAA
	81	GATGGCGCCCGTTGATAGGTATGG	CCATACCTATCAACGGGCGCCATC
	82	ATGAGAATCGCCGGCAATCTGCTA	TAGCAGATTGCCGGCGATTCTCAT
30	83	ATTTGCACTGACCGCAGGCTCGTG	CACGAGCCTGCGGTCAGTGCAAAT
	84	CAGGGAGAACGGTTAAGTTCCCGT	ACGGGAACCTAACC GTTCTCCCTG
	85	AGGCCGGCGATCGAGGAGTTTGGT	ACCAAACCTCTCGATCGCCGGCCT
	86	ACACGGTGGTCTCTGATAGCGACC	GGTCGCTATCAGAGACCACCGTGT
	87	GTGCAACGCCGAGGACTTCCATCA	TGATGGAAGTCTCGGCGTTGCAC
35	88	TCGGTGCCTGATAGCCATTCCGAT	ATCGGAATGGCTATCAGGCACCGA
	89	TGAAATACCACACAGCCAATTGGC	GCCAATTGGCTGTGTGGTATTTCA
	90	GCATCGTGACATGACTGCCGCGA	TCGCGGCAGTCATGTACACGATGC
	91	CAGTGTTCTAACGGCGCGCGTGAA	TTACGCGCGCCGTTAGAACACTG
	92	CGCTTGCAACGTTGCACCTACTCT	AGAGTAGGTGCAACGTTGCAAGCG
40	93	CGAAAACTAGTGGGCTCGCCGCG	CGCGGCGAGCCCACTAGTTTTTCG
	94	CTTTCAGGGGAAC TGCCGGAGTCG	CGACTCCGGCAGTTCCCTGAAAG

	95	TTGTGGCCTTCTTGTAAGGCACG	CGTGCCTTTACAAGAAGGCCACAA
	96	TCCACGAACGGCGACCCGTTGTCT	AGACAACGGGTGCGCGTTTCGTGGA
	97	CGACCTTGACGAAACCTAACGAG	CTCGTTAGGTTTCGTGCAAGGTCG
	98	GTGCAGCTTCACGAGCCAGCCTGA	TCAGGCTGGCTCGTGAAGCTGCAC
5	99	CGCTTTCGTGCGAATAGACGATGA	TCATCGTCTATTGCGACGAAAGCG
	100	TGCGCTTACAGGCTCCTAGTGGTC	GACCACTAGGAGCCTGTAAGCGCA
	101	CACGCGCTTAGTCGCGATCGCATA	TATGCGATCGCGACTAAGCGCGTG
	102	CGGAGGGAGGGAGCTAGCCTTCGA	TGGAAGGCTAGCTCCCTCCCTCCG
	103	GCATCCGGCCTGTTGATGACGCCT	AGGCGTCATCAACAGGCCGGATGC
10	104	AGGCCAATCGATCTTATTGCCGAG	CTCGGCAATAAGATCGATTGGCCT
	105	CCTTCCAATGATTGCATACGCCCA	TGGGCGTATGCAATCATTGGAAGG
	106	AACACTTGATCAGGCGGGTCTGCT	AGACGACCCGCGCTGATCAAGTGTT
	107	TGGAATCAAGCCGTAAAGGACAG	CTGTCTTTACGGCCTTGATTCCA
	108	GCTCCCGTAACCTGTCCACCAGTG	CACTGGTGGACAGGTTACGGGAGC
15	109	AGTGGTGAATGGCCGCTACCCTGA	TCAGGGTAGCGGCCATTCACTACT
	110	TGTTGAAGCGAGCTAAACGGCCA	TGGCCGTTTTAGCTCGCTTCAACA
	111	CAGCGCTCCAGAATTGACAGCAAT	ATTGCTGTCAATTCTGGAGCGCTG
	2	TTGGAAGCGCACGTCCCTTTTCAA	TTGAAAAGGGACGTGCGCTTCGAA
	3	AACGCGTGGGGAATGGGACATCAA	TTGATGTCCCATTCCCCACGCGTT
20	114	CACGAGATACCGGCGTAAGGGTGG	CCACCCTTACGCCGGTATCTCGTG
	115	CTACGGCAAACGTGTGGAATGGGT	ACCCATTCCACACGTTTGCCGTAG
	116	GTAGGGCGATGACGGGCGAACTAC	GTAGTTCGCCCCTCATCGCCCTAC
	117	AATCGACCTCCGCACACATTCGCA	TGCGAATGTGTGCGGAGGTCGATT
	118	GAGTCAGCATGGCGGCGGAGATTC	GAATCTCCGCCGCCATGCTGACTC
25	119	AGATAAAGACGCTGGCAACACGGG	CCCGTGTTGCCAGCGCTTTATCT
	120	GGTACCTCAACGCGAACCATTGT	ACAAGTGGTTGCGGTTGAGGTACC
	121	AAGCGATGGCTACCCAAGAGCGAT	ATCGCTCTTGGGTAGCCATCGCTT
	122	AGAGCTTATGCAGAACCAGGCGCC	GGCGCCTGGTTCTGCATAAGCTCT
	123	ATCGGTCTCACGCAGGGTTGGATA	TATCCAACCCTGCGTGAGACCGAT
30	124	TAGGTTGCCCGCCAGAAGAAACAT	ATGTTTCTTCTGGCGGGCAACCTA
	125	CGGTGCTGTTGCAAAAGCCTGTAG	CTACAGGCTTTTGCAACAGCACCG
	126	TGATGAAAGTTTGCGGCAGGACAC	GTGTCCTGCCGCAAACTTTCATCA
	127	GTTGAGTGCAGGATGCAGCGATAG	CTATCGCTGCATCCTGCACTCAAC
	128	AACATTGCGCGGTCCACCAGGGTT	AACCCTGGTGGACCGCGCAATGTT
35	129	GGGCAGTTAGAGAGGGCCAGAAGT	ACTTCTGGCCCTCTCTAACTGCC
	130	TCGAGCTGGTCCCGTGAACGTGT	ACACGTTACGGGGACCAGCTCGA
	131	GTCTTGGGGGCCGCTTAGTGAAAA	TTTTCACTAAGCGGCCCCCAAGAC
	132	ACTGTTGGCTTGCTCTCATGTCCA	TGGACATGAGAGCAAGCCAACAGT
	133	AGGACCATTGCGAAGGCGAAGATA	TATCTTCGCCCTCCGAATGGTCCT
40	134	CTTGGGAGGCATCCGCTATAAGGA	TCCTTATAGCGGATGCCTCCCAAG
	135	AATAAACGGAACGCACCGCTACAG	CTGTAGCGGTGCGTTCCGTTTATT



	136	TTGTACGTGCGGTCCCCATAAGCA	TGCTTATGGGGACCGCACGTACAA
	137	CGCACCAAAGTGAAGTTTCCAGAC	GTCTGGGAAAGTCAAGTTTGGTGCG
	138	ACCTGATCGTTCCCCTATTGGGAA	TTCCAATAGGGGAACGATCAGGT
5	139	GGAACAGAGGCGAGGGGACTGAGC	GCTCAGTCCCTCGCCTCTGTTCC
	140	CCCTGCCTTGGCGTGTGGGCTTAT	ATAAGCCGACACGCCAAGGCAGGG
	141	ACTCTGACACGCCAACTCCGGAAG	CTTCCGGAGTTGGCGTGTGAGAGT
	142	CTGACGGTTTTTCATTGGCGTGCC	GGCAGCCGAATGAAAACCGTCAG
	143	TGCGGTGGTTCATTGGAGCTGGCC	GGCCAGCTCCAATGAACCACCGCA
10	144	GCATGGCCAACTAGTGACTCGCAA	TTGCGAGTCACTAGTTGGCCATGC
	145	AGGCCGTAAAGCGAATCTCACCTG	CAGGTGAGATTCGCTTTACGGCCT
	146	CGAATATTATGCCGAGAATCCGCG	CGCGGATTCTCGGCATAATATTCG
	147	ACAGACGAGCTCCCAACCACATGA	TCATGTGGTTGGGAGCTCGTCTGT
	148	GGACGGTTTGTGCTGGATTGTCTG	CAGACAATCCAGCACAAACCGTCC
15	149	AAAGGCTATTGAGTTGGTTGGGCG	CGCCCAACCAACTCAATAGCCTTT
	150	GATGGCCTATTCCGAGATCGGGCC	GGCCCGATCTCCGAATAGGCCATC
	151	GATCCAGTAGGCAGCTTCATCCCA	TGGGATGAAGCTGCCTACTGGATC
	152	AATAACTCGCGCGGGTATGCTTCT	AGAAGCATACCCGCGCGAGTTATT
	153	GGAGGAGGTTTGTCTCGGAAAGCA	TGCTTTCCGAGACAAACCTCCTCC
20	154	CTTTGGTATGGCACATGCTGCCCG	CGGGCAGCATGTGCCATACCAAAG
	155	AGAAAGGCTCGAGCAACGGGAACT	AGTTCCCGTTGCTCGAGCCTTTCT
	156	AATCTACCGCACTGGTCCGCAAGT	ACTTGCGGACCAAGTCCGGTAGATT
	157	CGTGGCGGCCACAGTTTTTGGAGG	CCTCCAAAAGTGTGGCCGCCACG
	158	TTGCAGTTCAATCCATACGCACGT	ACGTGCGTATGGATTGAACTGCAA
25	159	GGCCCAAAGCCCCAGACCATTTTA	TAAAATGGTCTGGGGCTTTGGGGCC
	160	CGCCTGTCTTTGTCTCCGGACAAT	ATTGTCCGGAGACAAAGACAGGCG
	161	TGAGGCAACAGGGGCCAAAACTA	TAGTTTTTGGCCCCTGTTGCCTCA
	162	AGCGGAAGTAGTCTCGGCTCGTC	GACGAGCCGAGGACTACTTCCGCT
	163	GGCCCCAAGGCTTAGAGATAGTGG	CCACTATCTCTAAGCCTTGGGGCC
30	164	GCACGTGAAGTTTAACCGCGATTTC	GAATCGCGGTTAAACTTCACGTGC
	165	AGCGGCAGAAACGTTTCTTGACGG	CCGTCAAGGAACGTTTCTGCCGCT
	166	TCGTGAGCAGACGAGATTGCACG	CGTGCAATCTCGTCTGCTCGACGA
	167	TCTTTGCCGCGTAACTGACTGCTT	AAGCAGTCAGTTACGCGGCAAAGA
	168	TTTATGTGCCAAGGGGTTAACCGA	TCGGTTAACCCCTTGGCACATAAA
35	169	TGTTACTGTGGTTCACGGCAGTCC	GGACTGCCGTGAACCACAGTAACA
	170	CGCGCCTCGCTAGACCTTTTATTG	CAATAAAAGGTCTAGCGAGGCGCG
	171	ACAAATGCGTGAGAGCTCCCAACT	AGTTGGGAGCTCTCACGCATTTGT
	172	CGCGCAGATTATAGACCCGAATGT	ACATTCCGGTCTATAATCTGCGCG
	173	CAAATAACGCCGCTGAATCGGCGT	ACGCCGATTACGCGGCGTTATTG
40	174	CCTTCGTGCATCGGTGATGATGTT	AACATCATCACCGATGCACGAAGG
	175	TGAACACGAGCAACACTCCAACGC	GCGTTGGAGTGTGCTCGTGTTCA
	176	CAGCAGATCCTTCGTAGCGGTCGT	ACGACCGCTACGAAGGATCTGCTG

	177	GGAACCTGGTGAGTTGTGCCTCAT	ATGAGGCACAACCTCACCAGGTTCC
	178	TCATAAGCGACAATCGCGGGCTTA	TAAGCCCGCGATTGTGCGTTATGA
	179	CCCAACGTCACTGAAGCTCACAGT	ACTGTGAGCTTCAGTGACGTTGGG
5	180	TGTCAGAGCCCGCGACTCAGACGG	CCGTCTGAGTCGCGGGCTCTGACA
	181	TACACGAAGCCTCTCCGTGGTCCA	TGGACCACGGAGAGGCTTCGTGTA
	182	CTCAGAAAGTCCTCGGCGAACTGGG	CCCAGTTCGCCGAGGACTTCTGAG
	183	ATCCTTTTATCTACTCCGCGGCGA	TCGCCGCGGAGTAGATAAAAGGAT
	184	AGGCGTGCAGCAACAGGATAAACC	GGTTTATCCTGTTGCTGCACGCCT
	185	ACTCTCGAGGGAGTCTCTGGCACA	TGTGCCAGAGACTCCCTCGAGAGT
10	186	TTGCCAGGTCCATCGAGACCTGTT	AACAGGTCTCGATGGACCTGGCAA
	187	TCCACTATAACTGCGGGTCCGTGT	ACACGGACCCGCAGTTATAGTGGA
	188	GCCCAGTCGGCTCTAACAAGTTCG	CGAACTTGTTAGAGCCGACTGGGC
	189	CGGAACGGATAATCGGCGTCAGGT	ACCTGACGCCGATTATCCGTTCCG
	190	TAAATAAGCGCCTGGCGGGAGGA	TCCTCCCGCCAGGCGCTTATTTTA
15	191	GCGCACTCGTGAAACCTTTCTCGC	GCGAGAAAGGTTTCACGAGTGCGC
	192	AGTTTGCCAGGTACTGGCAAGTGC	GCACTTGCCAGTACCTGGCAAACCT
	193	ACAACGAGGGATGTCCAGCGGCAT	ATGCCGCTGGACATCCCTCGTTGT
	194	TTCGCAGCACCCGCTAGGTACAGT	ACTGTACCTAGCGGGTGCTGCGAA
	195	TAACCCGATTTTTGCGACTCTGCC	GGCAGAGTCGCAAAAATCGGGTTA
20	196	CGTCGCATTGCAAGCGTAGGCTTG	CAAGCCTACGCTTGCAATGCGACG
	197	GAGCTGACGTCAACATCAGAGGAA	TTCTCTGATGGTGACGTCAGCTC
	198	GGAGGCTGGGGGTGCGCTTAAGT	ACTTAAGCGCGACCCCCAGCCTCC
	199	TTGTGGGAACCGCACTAGCTGGCT	AGCCAGCTAGTGCGGTTCCACAA
	200	CCCTCGCACTGTGTTACCCCTCTT	AAGAGGGTGAACACAGTGCGAGGG
25	201	TCATTGACTCGAATCCGCACAACG	CGTTGTGCGGATTCGAGTCAATGA
	202	ACAGGGGTGGCCTTCGTACGTAC	GTACGTACGAAGGCCAACCCTGT
	203	AGGCCGTGCAACATCACACAGGAT	ATCCTGTGTGATGTTGCACGGCCT
	204	GGGCCGTGGTCACGTAATATTGGC	GCCAATATTACGTGACCACGGCCC
	205	GCGCGGACATGAAACGACAAGGCC	GGCCTTGTCGTTTCATGTCCGCGC
30	206	CTTATTGGGTGCCGGTGTGCGATT	AATCCGACACCGGCACCCAATAAG
	207	GGGGCGGTTACCAAAAAATCCGAT	ATCGGATTTTTTGGTAACCGCCCC
	4	CCGTCGCATACCGGCTACGATCAA	TTGATCGTAGCCGGTATGCGACGG
	5	ATGGCCGTGCTGGGGACAAGTCAA	TTGACTTGTCGCCAGCACGGCCAT
	210	ACGAAAAAAGTGTCGGATCCCCT	AGGGGATCCGCACACTTTTTTCGT
35	211	CCAAGTACACCGCACGCATGTTTA	TAAACATGCGTGCGGTGTACTTGG
	212	ATCGTGCGTGGAGTGTGCGATCTA	TAGATGCGCACTCCACGCACGAT
	213	TCCAGATACCGCCCCGAACTTTGA	TCAAAGTTCGGGGCGGTATCTGGA
	214	TCTGCTGGCAGCACGTGAAGTGGC	GCCACTTCACGTGCTGCCAGCAGA
	215	TTGAAATTGCTCTGCCGTGAGTCA	TGACTGACGGCAGAGCAATTTCAA
40	216	AGTCAGGCGAGATGTTCAAGCAGC	GCTGCCTGAACATCTCGCCTGACT
	217	ACAAGCCGACGTTAAGCCCGCCCA	TGGGCGGGCTTAACGTGCGCTTGT

	218	CCCTAATGAGGCCAGTAACCTGCA	TGCAGGTTACTGGCCTCATTAGGG
	219	GTGAGACACACATCCCCTCCAATG	CATTGGAGGGGATGTGTGTCTCAC
	220	CGACGGATGCAGAGTTCAGTGGTC	GACCACTGAACTCTGCATCCGTCG
5	221	CCCGCATGCCTGGCGGTATTACAA	TTGTAATACCGCCAGGCATGCGGG
	222	TTAGCAAAGCGGGCGCCGTTAGCAA	TTGCTAACGGCGCCGCTTTGCTAA
	223	CCCGACACGGGTCAGCGTAATAAT	ATTATTACGCTGACCCGTGTCGGG
	224	GCGACGGCCCTGAGGTATGTCGTC	GACGACATACCTCAGGGCCGTCGC
	225	CAAAAGTGTGTTCCCTTGCGCTTG	CAAGCGCAAGGGAACACACTTTTG
	226	TCTCGAAGCACAGCCCAGTTATTG	CAATAACCGGGCTGTGCTTCGAGA
10	227	ATGCTAACCGTTGGCCATGGAAT	AGTTCCATGGCCAACGGTTAGCAT
	228	CTTGCGGAGTGTTAGCCCAGCGGT	ACCGCTGGGCTAACACTCCGCAAG
	229	TGCTCCCTAGGCGCTCGGAGGAGT	ACTCCTCCGAGCGCCTAGGGAGCA
	230	CCAATGCCTTTGAGTAAGCGATGG	CCATCGCTTACTCAAAGGCATTGG
	231	AGCAGATAACGTCCAATGACGCC	GGCGTCATTGGGACGTTATCTGCT
15	232	TTGACCATTACGTGTTGCGCCCAT	ATGGGCGCAACACGTAATGGTCAA
	233	TCGCGTATTTGCGGAATTCGTCTG	CAGACGAATTCCGCAAATACGCGA
	234	CTGCGTGTCAACAATGTCCCGCAG	CTGCGGGACATTGTTGACACGCAG
	235	TCTGGTGCCACGCAAGGTCCACAG	CTGTGGACCTTGCGTGGCACCAGA
	236	CTCCGGGAGGTCACTTAATTGCGG	CCGCAATTAAGTGACCTCCCGGAG
20	237	TTTTCGTGATTGCCCGGAGGAGGC	GCCTCCTCCGGGCAATCACGAAAA
	238	TCGGGATGTAGCTGGGGCTACCGG	CCGGTAGCCCCAGCTACATCCCGA
	239	CGAGCCAACGCAACACGTCCTTG	CAAGGACGTGTTTGCCTTGGCTCG
	240	GCAAAGCCTTTGTGGGGCGGTAGT	ACTACCGCCCCACAAAGGCTTTGC
	241	ATTCGACCGGAAATGAGGTCTTCG	CGAAGACCTCATTTCCGGTCAAT
25	242	TTGCTTGCTGAGTTGCTCTGTTC	GAACAGAGCAACTCAGCAAGCGAA
	243	CGCGTGAAGACCCCATTCCCGAGT	ACTCGGGAATGGGGTCTTCACGCG
	244	AACCGTATTCGCGGTCACTTGTGG	CCACAAGTGACCGCGAATACGGTT
	245	GGGGCCAACCGTTTCGAGGCGTAT	ATACGCCTCGAAACGGTTGGCCCC
	246	TTGCGCTGGCAGTCCAAACGGCTT	AAGCCGTTTGGAAGTCCAGCCGAA
30	247	GGGTGTGGTTAGAATGCACGGTTC	GAACCGTGCAATTCTAACCACACCC
	248	GCGAGGACCGAACTAGACAAACGG	CCGTTTGTCTAGTTCGGTCCTCGC
	249	ACGCACGCGTGACCGAAGTTGCTG	CAGCAACTTCGGTCACGCGTGCGT
	250	TAAAGGTCGCTTTGAAAGGGGGA	TCCCCCTTTCAAAGCGACCTTTTA
	251	TGCGATCGCTAACTGCTGGGACAA	TTGTCCCAGCAGTTAGCGATCGCA
35	252	GGAGGTATAAGCGGAGCGGCCTCA	TGAGGCCGCTCCGCTTATACCTCC
	253	ATGCTGACATGTCGTGCACCTCGT	ACGAGGTGCACGACATGTCAGCAT
	254	TGTGGTTAAAGCGTCCGTTCAACG	CGTTGAACGGACGCTTTAACCACA
	255	CGTTCACACCGGCGTAAGCTGCGT	ACGCAGCTTACGCCGGTGTGAACG
	256	CCTATCCCGGCGAGAACTTCTGTG	CACAGAAGTTCTCGCCGGGATAGG
40	257	GTCTGCACTCACGCAGCGGAGGGA	TCCCTCCGCTGCGTGAGTGCAGAC
	258	GCACGAGTTGGTGCTCGGCAGATT	AATCTGCCGAGCACCAACTCGTGC

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259	AACGTCGCACGACACACGTTGTC	GACGAACGTGTGTCGTGCGACGTT
260	ATGCGCGCTTATCCTAGCATGGTC	GACCATGCTAGGATAAGCGCGCAT
261	TCACGTTTTCTGTCTCGACATGAGG	CCTCATGTCGAGACGAAAACGTGA
262	TGTGCCTCATCCTTAGGATACGGC	GCCGTATCCTAAGGATGAGGCACA
263	AGGTGGTGTGGGTCAACCGCTTTA	TAAAGCGGTTGACCCACACCACCT
264	CTGGATCGAAGGGACTGCAAGCTC	GAGCTTGCAGTCCCTTCGATCCAG
265	TAGATCAACTCGCGTACGCATGGA	TCCATGCGTACGCGAGTTGATCTA
266	GATCCTGCGGAGAAGAGAGTGACAG	CTGCACTCTCTTCTCCGCAGGATC
267	TACGTGTGGAGATGCCCCGAACCG	CGGTTGCGGGCATCTCCACACGTA
268	GCGCTATGTCAATCGTGGGCGTAG	CTACGCCCACGATTGACATAGCGC
269	AGCGAGGTTTCTAGCGTCGACACC	GGTGTGACGCTAGAAACCTCGCT
270	ACCCAGGTTTTGCCGTTGTGGAAT	ATTCCACAACGGCAAAACCTGGGT
271	CCCTGTTAACGGCTGCGTAGTCTC	GAGACTACGCAGCCGTTAACAGGG
272	AGGCCGATTTACCCGCCAATTGC	GCAATTGGCGGGTGAAATCGGCCT
273	GAGCCCTCACTCCTTGCCCTTTGA	TCAAAGGGCAAGGAGTGAGGGCTC
274	GGGTGGACATCCGCCTCGCAGTCA	TGACTGCGAGGCGGATGTCCACCC
275	GATGGCTGAGAACCCTGCTACGAT	ATCGTAGCACGGTTCTCAGCCATC
276	TCGACGTTAGGAGTGCTGCCAGAA	TTCTGGCAGCACTCCTAACGTCGA
277	CGAATGGGTCTGGACCTTGACATAG	CTATGCAAGGTCCAGACCCATTG
278	GTGCACCAGACATTCGAACTCGGA	TCCGAGTTCGAATGTCTGGTGAC
279	AGAGGCCCGTATATCCCATCCAT	ATGGATGGGATATACGGGGCCTCT
280	AACGCCTGTTCAAGCATCAGCGG	CCGCTGATGCTCTGAACAGGCGTT
281	AAGGCTCAACACGCCTATGTGCGC	GCGCACATAGGCGTGTGAGCCTT
282	AGTCCGTGTTGCCAGATTGGCTCG	CGAGCCAATCTGGCAACACGGACT
283	ATGTCCCATGTAAAGACGCGTGTG	CACACGCGTCTTTACATGGGACAT
284	ATGGAGTCTGCTCACGCCCAAAGG	CCTTTGGGCGTGAGCAGACTCCAT
285	CGGCCTCCAACAAGGAGCACTAAC	GTTAGTGCTCCTTGTTGGAGGCCG
286	CAGAGCCGTGGCAACATTGCGAGC	GCTCGCAATGTTGCCACGGCTCTG
287	TCATTTGAATGAGGTGCGCACCGG	CCGGTGCGCACCTCATTCAAATGA
288	GACGTACCGGAAGCGCCGTATAAA	TTTATACGGCGCTTCCGGTACGTC
289	ATGCGAGCAATGGGATCCGGATTG	GAATCCGGATCCCATTGCTCGCAT
290	AGAGTGAGGCCTCCCTGACCAGTG	CACTGGTCAGGGAGGCCTCACTCT
291	CGCACCGTAAGTAGATTTGCCCGC	GCGGGCAAATCTACTTACGGTGCG
292	TGAACCTTTGAGCACGTCGTGCGC	GCGCACGACGTGCTCAAAGGTTCA
293	TCCGCCTTTTGGTTACCTCGAAG	CTTCGAGGTAACCAAAAAGGCGGA
294	GAACGCCAACGGCACTAACACATC	GATGTGTTAGTGCCGTTGGCGTTC
295	CCGACAGCAGCCAAGACGTCCAG	CTGGGACGTCTTGCTGCTGTGCG
296	CATAAAAAACCTGGGGCTCTGCG	CGCAGAGCCCCAGGTTTTTTATG
297	TGCCAACTGTGCAGACCGGACTTA	TAAGTCCGGTCTGCACAGTTGGCA
298	GGCGAAAGAGCGAAACCGGCTCGT	ACGAGCCGGTTTCGCTCTTTCGCC
299	GGGATGCGTATTTTAGCGAACACG	CGTGTTGCTAAAATACGCATCCC

	300	TGGGATTCAGCGACCAGTACGCGA	TCGCGTACTGGTCGCTGAATCCCA
	301	CCCGATATTCGCCCCGGCCTATTTCG	CGAATAGGCCGGGCGAATATCGGG
	302	CGAGAAGATGCCTCACGCAACCAA	TTGGTTGCGTGAGGCATCTTCTCG
	303	AACCTTGACCCGTGGATGACGCTA	TAGCGTCATCCACGGGTCAAGGTT
5	6	TTGCAACGGGCTGGTCAACGTCAA	TTGACGTTGACCAGCCCGTTGCAA
	7	CGCATAGGTTGCCGATTTTCGTCAA	TTGACGAAATCGGCAACCTATGCG
	306	GCTTCCGGATGAACGGGATGGTTG	CAACCATCCCGTTCATCCGGAAGC
	307	CCCTCCATGTTCTTCGAACGGTTT	AAACCGTTTGAAGAACATGGAGGG
	308	TTGATGGGCGGCAATGCTCTTGCT	AGCAAGAGCATTGCCGCCCATCAA
10	309	ATTGTGAGATGCGCCAAATTCGCC	GGGGAATTTGGCGCATCTCACAAT
	310	TCAGCACAGCCAGACGGTCAACTT	AAGTTGACCGTCTGGCTGTGCTGA
	311	ACTCCACTCCTCGGTGGCAAACCTA	TAGTTTGCCACCGAGGAGTGAGT
	312	TCTGGGCATGCCTGGACGGAGACG	CGTCTCCGTCCAGGCATGCCGAGA
	313	TCTCAACTCCGGTACGACGAAACA	TGTTTCGTCTGACCGGAGTTGAGA
15	314	TTGCGTGGTCAAAGGCGCAACGTG	CACGTTGCGCCTTTGACCACGCAA
	315	AGACAGCGATCCGCGGCTCATGAT	ATCATGAGCCGCGGATCGCTGTCT
	316	CGCGTCTCTAACTGAGAGCAGCCA	TGGCTGCTCTCAGTTAGAGACGCG
	317	AGGCGCACATGTACGGACATTCAG	CTGAATGTCCGTACATGTGCGCCT
	318	GATGAGTGGCACGTGCGTGTGTAA	TTACACACCGACGTGCCACTCATC
20	319	TGATCCATATTGTCTGGACGTTGCG	CGCAACGTCCGACAATATGGATCA
	320	ACCTGCCGGGAGTTCATAGGCTAG	CTAGCCTATGAACTCCCGGCAGGT
	321	AGCATTGGCGTTTTTCCGCAACGA	TCGTTGCGGAAAAACGCCAATGCT
	322	GGTAATATTCAGCGCGACCGCTCA	TGAGCGGTCTGCGCTGAATATTACC
	323	ATAGCGTACGACGAGGTGACGCGC	GCGCGTCACCTCGTCGTACGCTAT
25	324	TAGGTCACGATGCGTTTGACGCTA	TAGCGTCAAACGCATCGTGACCTA
	325	ACTGCCCCGTACCTCTGGTTCTGGC	GCCAGAACCAGAGGTACGGGCAGT
	326	CCTTTGGCCTGAAGTTGTCTGAGC	GCTACGACAACCTCAGGCCAAAGG
	327	GTGCCCCACGAGCGTATCGTTGTA	TACAACGATACGCTCGTGGGGCAC
	328	AGGCGCTACGTGGGCCTGGAGCAA	TTGCTCCAGGCCACGTAGCGCCT
30	329	GGGTGCTACCATTGCATTAGTCCG	CGGACTAATGCAATGGTAGACCCC
	330	ACCACGCGCGTACGTGTAACCGAG	CTCGGTTACACGTACGCGCGTGGT
	331	CCATGATGCATTGGGTGCATTAG	CTAAATGCACCCAATGCATCATGG
	332	GGTCCGGCCCTACGAAACGTTTCA	TCGAACGTTTTCGTAGGGCCGGACC
	333	CCGTGTGGCTGGAGATTCGTGTGA	TCACACGAATCTCCAGCCACACGG
35	334	GTTAGGGCGACGCATATTGGCACA	TGTGCCAATATGCGTCGCCCTAAC
	335	GGGTCAGTCAGGTGCGTTAGGATC	GATCCTAACGCACCTGACTGACCC
	336	GCCGTGAAGTCGAATGCAGATCGA	TCGATCTGCATTGCACTTACGGC
	337	GCCACCACCCAGTGCATTGAGGTA	TACCTGAATGCACTGGGTGGTGGC
	338	GAGCTTAGTTTGCGGTATCGGGC	GCCCGATGACCGCAAACCTAAGCTC
40	339	TGTTTGCCGCCATTAGGGAGTAAC	GTTACTCCCTAATGGCGGCAAACA
	340	GCTCCGCTGGATGTGCCGGTTTAG	CTAAACCGGCACATCCAGCGGAGC

	341	CGGTAGCATGCGAGATCCCTGTTA	TAACAGGGATCTCGCATGCTACCG
	342	CTACGCTCTACCAGTTGCCTGCGA	TCGCAGGCAACTGGTAGAGCGTAG
	343	GTGCCTCCTGCTGTATTTGCCAAG	CTTGGCAAATACAGCAGGAGGCAC
5	344	TTGCGACTCGACTTGGACGAGTAG	CTACTCGTCCAAGTCGAGTCGCAA
	345	TCTGGGAGCTGTTTACTCCAGCCA	TGGCTGGAGTAAACAGCTCCCAGA
	346	TGCACGCGGAACTCCCTTTACCAT	ATGGTAAAGGGAGTTCCGCGTGCA
	347	TGGCAGCAAATGAATCGAAAGCAC	GTGCTTTCGATTCATTTGCTGCCA
	348	AACTGGTGACGCGGTACAGCGAAG	CTTCGCTGTACCGCGTCACCAGTT
10	349	AGACGATTACGCTGGACGCCGTCG	CGACGGCGTCCAGCGTAATCGTCT
	350	ATGCCCTCCTTCATGGAAAGGGTT	AACCCTTTCCATGAAGGAGGGCAT
	351	ATTCTCGGAGCGTATGCGCCAGAA	TTCTGGCGCATACGCTCCGAGAAT
	352	ATAGCGGAGTTTGGGTACGCGAAC	GTTGCGGTACCCAAACTCCGCTAT
	353	ACCTACGCATACCGCTTGGCGAGG	CCTCGCCAAGCGGTATGCGTAGGT
15	354	GATTACCTGAATGGCCAAGCGAGC	GCTCGCTTGGCCATTCAAGTAATC
	355	CCTGTTAGCATCACGGCGCTTAGG	CCTAAGCGCCGTGATGCTAACAGG
	356	CGGAATGATGCGCTCGACAACGCT	AGCGTTGTCGAGCGCATATTCCG
	357	TGAGAGAGGCGTTGGTTAAGGCAA	TTGCCTTAACCAACGCCTCTCTCA
	358	AAGCAGGCGAAGGGATACTCCTCG	CGAGGAGTATCCCTTCGCCTGCTT
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	360	AAGCAATTTGGCCTCGTTTGTGA	TCACAAAACGAGGCCAAATTGCTT
	361	GCTGGTTGCGGTAGGATCGCATAT	ATATGCGATCCTACCGCAACCAGC
	362	TTGTGAATCCGTTCTGTCCCGAC	GTCGGGGACAGAACGGATTACAA
	363	TGGGCTCCTCTGAGGCGAGATGGC	GCCATCTCGCCTCAGAGGAGCCCA
25	364	GGATAGAGTGAATCGACCGGCAAC	GTTGCCGGTCGATTCACTCTATCC
	365	TGCACCGAACGTGCACGAGTAATT	AATTACTCGTGACGTTCCGGTGCA
	366	GCCAGTATTCTCGGGTGTGGACG	CGTCCAACACCCGAGAATACTGGC
	367	TCGCTACCTAAGACCGGGCCATAC	GTATGGCCCGGTCTTAGGTAGCGA
	368	TGGCATTGACGAGCAGCAGTCAGT	ACTGACTGCTGCTCGTCAATGCCA
30	369	CGCGTCCCAGCGCCCTTGGAGTAT	ATACTCCAAGGGCGCTGGGACGCG
	370	ATGAAGCCTACCGGGCGACTTCGT	ACGAAGTCGCCCGGTAGGCTTCAT
	371	CCAGACAGATGGCCTGGAACCATG	CATGGTTCCAGGCCATCTGTCTGG
	372	TGGCGTGGGACCATCTCAAAGCTA	TAGCTTTGAGATGGTCCCACGCCA
	373	CCGCATGGGAACACGTGTCAAGGT	ACCTTGACACGTGTTCCCATGCGG
35	374	GCCCACTCGTCAGCTGGACGTAAT	ATTACGTCCAGCTGACGAGTGGGC
	375	ATTACGGTCGTGATCCAGAAAGCG	CGCTTTCTGGATCACGACCGTAAT
	376	TGCGAGGTGAGCACCTACGAGAGA	TCTCTCGTAGGTGCTCACCTCGCA
	377	GGGCCGCATTCTTGATGTCCATT	GAATGGACATCAAGAATGCGGCCC
	378	CCTCGGATGTGGGCTCTCGCCTAG	CTAGGCGAGAGCCCACATCCGAGG
40	379	TAGGCATGTTGGCGTGAGCGCTAT	ATAGCGCTCACGCCAACATGCCTA
	380	CGATACGAACGAGGATGTCCGCCT	AGGCGGACATCCTCGTTCGTATCG
	381	TACGCCGGTTAGCACGGTGCGCTA	TAGCGCACCGTGCTAACGGCGCTA

	382	CATACGATGTCCGGGCCGTGTCGC	GCGACACGGCCCGGACATCGTATG
	383	ATCCGCAGTTGTATGGCGCGTTAT	ATAACGCGCCATACAACCTGCGGAT
	384	GGGTAAGGGACAAAGATGGGATGG	CCATCCCATCTTTGTCCCTTACCC
5	385	ATTGGAGTGTTTTGGTGAATCCGC	GCGGATTCACCAAAACACTCCAAT
	386	GAACCGAGCCAACGTATGGACACG	CGTGTCCATACGTTGGCTCGGTTTC
	387	GCCGTCAAGCTTAAGGTTTTGGGC	GCCCAAAACCTTAAGCTTGACGGC
	388	ACCTGCTTTTGGGTGGGTGATATG	CATATCACCCACCCAAAAGCAGGT
	389	AATCGTGGGCGCAGCAAACGTATA	TATACGTTTGCTGCGCCCACGATT
10	390	GTCGCCGGATTGCTCAGTATAAGC	GCTTATACTGAGCAATCCGGCGAC
	391	ACCCGTCGATGCTTCCTCCTCAGA	TCTGAGGAGGAAGCATCGACGGGT
	392	ATCCGGGTGGGCGATACAAGAGAT	ATCTCTTGATCGCCACCCGGAT
	393	TTCCGCATGAGTCAGCTTTGAAAA	TTTTCAAAGCTGACTCATGCGGAA
	394	GCAAAGTCCCACTGGCAAGCCGAT	ATCGGCTTGCCAGTGGGACTTTGC
15	395	CGACCTCGGCTTCATCGTACACAT	ATGTGTACGATGAAGCCGAGGTCG
	396	CTCATGAGCGCAGTTGTGCGTGAG	CTCACGCACAACCTGCGCTCATGAG
	397	CAGATGAAGGATCCACGGCCGGAG	CTCCGGCCGTGGATCCTTCATCTG
	398	TCAAAGGCTCTTGGATACAGCCGT	ACGGCTGTATCCAAGAGCCTTTGA
	399	TCCGCTAATTTCCAATCAGGGCTC	GAGCCCTGATTGGAAATTAGCGGA
20	8	CCGTTTGCGGTGCTCCTTGCTCAA	TTGAGCAAGGACGACCGCAAACGG
	9	TTGCGTTTCGTGGCTGCACTTCAA	TTGAAGTGCAGCCACGAAAGCGAA
	402	CTTAGTTGGGGCGCGGTATCCAGA	TCTGGATACCGCGCCCCAACTAAG
	403	GCTCTAATGCCGTGGAGTCGGAAC	GTTCCGACTCCACGGCATTAGAGC
	404	CCGATTACAAATTGACTGACCGCA	TGCGGTCAATTTGTAATCGG
25	405	AGACGTACGTGAGCCTCCCGTGTC	GACACGGGAGGCTCACGTACGTCT
	406	AATGGAGCGATACGATCCAACGCA	TGCGTTGGATCGTATCGCTCCATT
	407	GGAGGCGCTGTACTGATAGGCGTA	TACGCCTATCAGTACAGCGCCTCC
	408	TGTTTTTGAATTGACCACACGGGA	TCCCGTGTGGTCAATTCAAAAACA
	409	CATGTCTGGATGCGCTCAATGAAG	CTTCATTGAGCGCATCCAGACATG
30	410	GCCCGCTAATCCGACACCCAGTTT	AACTGGGTGTCGGATTAGCGGGC
	411	CCATTGACAGGAGAGCCATGAGCC	GGCTCATGGCTCTCCTGTCAATGG
	412	GAATCACCGAATCACCGACTCGTT	AACGAGTCGGTGATTCGGTGATTC
	413	AACCAGCCGCAGTAGCTTACGTCG	CGACGTAAGCTACTGCGGCTGGTT
	414	TTTTCTGAGGGACACGCGGGCGTT	AACGCCCCGCGTGTCCTCAGAAAA
35	415	GGTGCTCCGTTTGATCGATCCTCC	GGAGGATCGATCAAACGGAGCACC
	416	CCGCTTAGGCCATACTCTGAGCCA	TGGCTCAGAGTATGGCCTAAGCGG
	417	TAAGACATACCGACGCCCTTGCCT	AGGCAAGGGCGTCGGTATGTCTTA
	418	GTTCCCGACGCCAGTCATTGAGAC	GTCTCAATGACTGGCGTCGGGAAC
	419	TAAAGTTTTGCGGAGGTGCGGCT	AGCCCGACCTCCGCGAAACTTTTA
40	420	CGGTCCAGACGAGCTGAGTTCGGC	GCCGAACTCAGCTCGTCTGGACCG
	421	CGGCGTAGCGGCTACGGACTTAAA	TTTAAGTCCGTAGCCGCTACGCCG
	422	GCTTGGATGCCCATGCGGCAAGGT	ACCTTGCCGCATGGGCATCCAAGC

	423	AGCGGGATCCCAGAGTTTCGAAAA	TTTTCGAAACTCTGGGATCCCGCT
	424	GAGCTTGAGAGCGAGGTCATCCTC	GAGGATGACCTCGCTCTCAAGCTC
	425	GCATCGGCCGTTTTGACCATATTC	GAATATGGTCAAAACGGCCGATGC
	426	CATAGCGCTGCACGTTTCGACCGC	GCGGTCGAAACGTGCAGCGCTATG
5	427	ACCCGACAACCACCAATTCAAAAA	TTTTTGAATTGGTGGTTGTCCGGT
	428	GCGAACACTCATAAGAGCGCCCTG	CAGGGCGCTCTTATGAGTGTTTCGC
	429	CCGCCGAGTGTAGAGAGACTCCGA	TCGGAGTCTCTCTACACTCGGCCG
	430	GACATCGGGAGCCGGAACATGAG	CTCATGTTTCCGGCTCCCGATGTC
	431	TCGTGTAGACTCGGCGACAGGCGT	ACGCCTGTGCCGAGTCTACACGA
10	432	ATGCGCATATACTGACTGCGCAGG	CCTGCGCAGTCAGTATATGCGCAT
	433	ACAAGCGAACCCGAGTTTTGATGA	TCATCAAACTCGGGTTCGCTTGT
	434	GCATGAGACTCCGCGAAGACATGT	ACATGTCTTCGCGGAGTCTCATGC
	435	TCCTACATGTCGCGTCACGATCAC	GTGATCGTGACGCGACATGTAGGA
	436	GACCGATCGCGAAGTCGTACACAT	ATGTGTACGACTTCGCGATCGGTC
15	437	GTCGCCAGGACTGGGCCGATGTGA	TCACATCGGCCAGTCCTGGCGAC
	438	ACCGATAAGACTTGCATCCGAACG	CGTTCGGATGCAAGTCTTATCGGT
	439	TCCATAACCAGTCCGAAGTGCCGG	CCGGCACTTCGGACTGGTTATGGA
	440	ACGCGCCCTGCATCTCGTATTTAA	TTAAATACGAGATGCAGGGCGCGT
	441	AGACCGCATCAATTGGCGCGTACC	GGTACGCGCCAATTGATGCGGTCT
20	442	AGAGGCTTGGCAAGTAGGGACCCT	AGGGTCCCTACTTGCCAAGCCTCT
	443	GCAATGGACGCCAGACGATACCGG	CCGGTATCGTCTGGCGTCCATTGC
	444	GCTGGACTTAGTCGTGTTCCGGCGG	CCGCCGAACACGACTAAGTCCAGC
	445	AGGCATCGTGCCGATTGCTCCCT	AGGGAGCAATCCGGCACGATGCQT
	446	TGCGCATGTGACGTTGAACAAAG	CTTTGTTCAACGTCGACATGCGCA
25	447	TTCCGGTACATCCGATGCCATAC	GTATGGCATCGGATGTGACCCGAA
	448	ACCCATCGCCGGAAGCGATGTTG	CAACATCGCTTTCGGCGATGGGT
	449	AAGCGCTGACTCGGCTAAGAATCA	TGATTCTTAGCCGAGTCAGCGCTT
	450	ACTTCCAAGTCCTTGACCGTCCGA	TCGGACGGTCAAGGACTTGGAAGT
	451	TCTCAATATTCCTGTAGTCGCCCA	TGGGCGACTACGGGAATATTGAGA
30	452	AACAGTTCCTCTTTTCTGCGCGC	GCGCCAGGAAAAAGAGGAAGTGT
	453	CGTCCTCCATGTTGTCACGAACAG	CTGTTCTGTGACAACATGGAGGACG
	454	TGCGCAGACCTACCTGTCTTTGCT	AGCAAAGACAGGTAGGTCTGCGCA
	455	ATGGACGGCTTCGCAGTCCTCCTT	AAGGAGGACTGCGAAGCCGTCCAT
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35	457	TGAACCCTGCCGCGAGCGATAACC	GGTTATCGCTCGCGGCAGGGTTCA
	458	GTTCTTGCGCGATGAATCAGGACC	GGTCCTGATTCATCGCGCAAGAAC
	459	AGGGTACGTGTGCGAGCTTCGCGT	ACGCGAAGCTGCGACACGTACCCT
	460	ACCCTTGCTCCGCCATGTCTCTCA	TGAGAGACATGGCGGAGCAAGGGT
	461	GGGACAAGGATTGAAGCTGGCGTC	GACGCCAGCTTCAATCCTTGTCCC
40	462	TGTCGTTGCTCCCGAGTACCATTG	CAATGGTACTCGGGAGCAACGACA
	463	GTTGTCCGAGACGTTTGTGTCAGC	GCTGACACAAACGTCTCGGACAAC



	464	GCTGGTGAACACTCACGAACCGCT	AGCGGTTCGTGAGTGTTCACCAGC
	465	GCAGACAGGGCAAATCGGTGCAAA	TTTGCACCGATTGCCCCTGTCTGC
	466	CCCATCACAACGAGTGGCGACTTT	AAAGTCGCCACTCGTTGTGATGGG
	467	GCTTCTACAGCTGGCGTGCTAGCG	CGCTAGCACGCCAGCTGTAGAAGC
5	468	GAATGTGTGCCGACCATTTCTAGCC	GGCTAGAATGGTCGGCACACATTC
	469	CCAGCGGAAGTTAGAGCTCTGTGG	CCACAGAGCTCTAACTTCCGCTGG
	470	TTTTTACCGACCACTCCATGTCCG	CCGACATGGAGTGGTCGGTAAAAA
	471	GCGGCTATGTGATGACGGCCTAGC	GCTAGGCCGTATCACATAGCCGC
	472	AGTACACGGGCGTGTTAGCGCTCC	GGAGCGCTAACACGCCCCGTGACT
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	474	CCAACTAACCAATCGCGCGGATGA	TCATCCGCGCGATTGGTTAGTTGG
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	476	CATCTTTCGCGGAGTTTATTGCGG	CCGCAATAAACTCCGCGAAAGATG
	477	CTTCGTCCGGTTAGTGCGACAGCA	TGCTGTGCGACTAACCGGACGAAG
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	479	CGCAGCAGCTGAACTCTAGCATTG	CAATGCTAGAGTTCAGCTGCTGCG
	480	AGGAGACATACGCCCAAATGGTGC	GCACCATTGTTGGCGTATGTCTCCT
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	484	AAACGCCGCCCTGAGACTATTGGG	CCAATAGTCTCAGGGCGGGCGTTT
	485	CTGAGTTGCCTGGAACGTTGGACT	AGTCCAACGTTCCAGGCAACTCAG
	486	CGGATGGGTTGCAGAGTATGGGAT	ATCCCATACTCTGCAACCCATCCG
	487	CTGACCTTTGGGGGTTAGTGCGGT	ACCGCACTAACCCCCAAAGGTCAG
25	488	GGAAATGAGAACCTTACCCCAGCG	CGCTGGGGTAAGGTTCTCATTTC
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	490	TGGAGAGAGACTTCGGCCATTGTT	AACAATGGCCGAAGTCTCTCTCCA
	491	TTGCGCTCATTGGATCTTGTGAGG	CCTGACAAGATCCAATGAGCGCAA
	492	AGCGCGTTAAAGCACGGCAACATT	AATGTTGCCGTGCTTTAACGCGCT
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	494	CGACTGATGTGCAACCAGCAGCTG	CAGCTGCTGGTTGCACATCAGTCG
	495	GGTTGCTCATACGACGAGCGAGTG	CACTCGCTCGTCGTATGAGCAACC
	10	GTCCAACGCGCAACTCCGATTCAA	TTGAATCGGAGTTGCGCGTTGGAC
	11	TTGCCGCACCGTCCGTATCTCAA	TTGAGATGACGGACGGTGCGGCAA
35	498	AGAACCTCCGCGCCTCCGTAGTAG	CTACTACGGAGGCGCGGAGGTTCT
	499	AAAGGAGCTTTCGCCCAACGTACC	GGTACGTTGGGCGAAAGCTCCTTT
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519	GCCACCTTTAGACGGCGGCTCTAG	CTAGAGCCGCGCTCTAAAGGTGGC
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521	TAGCTCGTGGCCCTCCAAGCGTGT	ACACGCTTGAGGGGCCACGAGCTA
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533	GTCACCAGGAGGGAAGTTTCACCC	GGGTGAAACTTCCCTCCTGGTGAC
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	546	TTATCGCGAGAGACGACCGTGTCC	GGACACGGTCGTCTCTCGCGATAA
	547	GACGCGACGTGAGTAGTGAAGCG	CGCTTCCACTACTCACGTCGCGTC
	548	ATGGTAGGGGCATTGGGCTTTCCT	AGGAAAGCCCAATGCCCCACCAT
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	550	GCAAACCCTGATTGAATCGTGCCC	GGGCACGATTCAATCAGGGTTTGC
	551	TAGCGTCTTGCGTGAAACCATGGG	CCCATGGTTTCACGCAAGACGCTA
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	555	TGATCCCGGACCGGCTAGACTAAT	ATTAGTCTAGCCGGTCCGGGATCA
	556	GGCCCCGACACTACAGGGTAATCA	TGATTACCCTGTAGTGTCGGGGCC
	557	GGCTCCAGGGCGAGATTATGAATG	CATTATAATCTCGCCCTGGAGCC
	558	CAAAATCCGATGGGCGGAAATTA	TAATTTTCCGCCCATCGGATTTTG
	559	CACAGGCGCATAGGGAGCAAGCTA	TAGCTTGCTCCCTATGCGCCTGTG
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	561	TGGTACGCGGTCCATAGCAAGTCG	CGACTTGCTATGGACCGCGTACCA
	562	GACGCTGTGGCTCGGAACTGTTT	GAACAGTTTCCGAGCCACAGCGTC
	563	CCTGGGTTGCGCCGCGTGGTAACTG	CAGTTACCACGCGGCGAACCCAGG
	564	TTCCCGCGTAGCCCAACAGCTATA	TATAGCTGTTGGGCTACGCGGGAA
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	566	AAAAATGGCACCGAAGTTGAGGCA	TGCCTCAACTTCGGTGCCATTTTT
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	568	ACGCACGTTTTTTGGCACGGTTAA	TTAACCGTGCCAAAAAACGTGCGT
	569	TGTCCATGACGTCGTTTCTCTGGT	ACCAGAGAAACGACGTCATGGACA
25	570	TCTCAGTCGGA CTGATGCCAGA	TCTGGCATA CGAGTCCGACTGAGA
	571	CTCCAAACGCACACATCAAGCATC	GATGCTTGATGTGTGCGTTTGGAG
	572	TTCAACCAAGCGGGGTGTTGCTGA	TCACGAACACCCCGCTTGTTGAA
	573	GGTGTCGGAGGGTGGTGACCTCGA	TCGAGGTCAACACCCTCCGACACC
	574	AGCGCTTTTGGTCATGATTTGCAA	TTGCAAATCATGACCAAAAGCGCT
30	575	CCGAGGACTTACGTCTGCCCAGGA	TCCTGGGCAGACGTAAGTCCTCGG
	576	GCCCAATCCAGTTCTTATGCGCCC	GGGCGCATAAGAACTGGATTGGGC
	577	CGGGTTAACCCACGCAAGTTATGA	TCATAACTTGCGTGGGTTAACCCG
	578	TGATTAGCGCTCAATACACGCGTG	CACGCGTGTATTGAGCGCTAATCA
	579	AAGGGCAGACCTTTGGTTCGACTG	CAGTCGAACCAAAGGTCTGCCCTT
35	580	GCGCCACAAGATTCACATGTCATT	AATGACATGTGAATCTTGTGGCGC
	581	GCCATGTTCAAGGGCCTTTGGAAG	CTTCGAAAGGCCCTTGAACATGGC
	582	CGCGGTGTTTTGTCTAGGTGCCGG	CCGGCACCTAGACAAAACACCGCG
	583	CAACATTGTGGTGGCACTCCATCC	GGATGGAGTGCCACCACAATGTTG
	584	CGATACGCGCCGGTTTGTAAATC	GATTTAACAAACCGGCGCGTATCG
40	585	GGCTATAAACGTGCGGACTGCTCC	GGAGCAGTCCGCACGTTTATAGCC
	586	TGGGTAAATCACTATTGCGCGGTT	AACCGCGCAATAGTGATTTACCCA

	587	GTCTTCATCGGCCCGCGCAAGCTA	TAGCTTGC GCGGGCCGATGAAGAC
	588	GCGACACACCCTGTACTCTGATGC	GCATCAGAGTACAGGGTGTGTCGC
	589	GTAGCAGGGTCCGCAAGACCAAGC	GCTTGGTCTTGCGGACCCTGCTAC
5	590	TCGCCAACGCAGGGTAACTGCCAT	ATGGCAGTTACCCTGCGTTGGCGA
	591	ACTCCGAAGCTTCGAGCGGCACGA	TCGTGCCGCTCGAAGCTTCGGAGT
	12	CATCGTCCCTTTTCGATGGGATCAA	TTGATCCCATCGAAAGGGACGATG
	13	GCACGGGAGCTGACGACGTGTCAA	TTGACACGTCGTCAGCTCCCCTGC
	594	ATCATCCACGCGCAGAGTGAAGAG	CTCTTCACTCTGCCGTGGGATGAT
	595	CGCTGGACTGGCCTATCCGAGTCG	C GACTCGGATAGGCCAGTCCAGCG
10	596	CGGTCTCAGCAAACTGTGCGAAA	TTTGCGACAGTGTTGCTGAGACCG
	597	CGAACGTTCTCCGATGTAATGGCC	GGCCATTACATCGGAGAACGTTCCG
	598	ATACCGTGCGACAAGCCCCTCTGA	TCAGAGGGGCTTGTCGCACGGTAT
	599	AGCTCATTCCCGAGACGGAACACC	GGTGTTCCGTCTCGGGAATGAGCT
	600	TTTCATGCGGCCGTTGCAAATCAT	ATGATTTGCAACGGCCGCATGAAA
15	601	ACTCGAACGGACGTTCAATTCCCA	TGGGAATTGAACGTCCGTTTCGAGT
	602	CTGCATGGTGTGGGTGAGACTCCC	GGGAGTCTCACCACACCATGCAG
	603	CCGCGAGTGTGGATGGCGTGTTGA	TCAACACGCCATCCACACTCGCGG
	604	AATGTGTGCGTCTTAAGCCGGGTG	CACCCGGCTTAGGACCGACACATT
	605	TAAGACGAGCCTGCACAGCTTGCG	CGCAAGCTGTGCAGGCTCGTCTTA
20	606	GGCGTGGGAGGATAAGACGATGTC	GACATCGTCTTATCCTCCCACGCC
	607	TGCTCCATGTTAGGAACGCACCAC	GTGGTGCGTTCCTAACATGGAGCA
	608	CGGTGTTGGTCGGA CTGACGACTG	CAGTCGTCAGTCCGACCAACACCG
	609	CCGCGCGTATCTATCAGATCTGGG	CCCAGATCTGATAGATACGCGCGG
	610	AAAGCATGCTCCACCTGGAGCGAG	CTCGCTCCAGGTGGAGCATGCTTT
25	611	ACTTGCATCGCTGGGTAGATCCGG	CCGGATCTACCCAGCGATGCAAGT
	612	TGCTTACGCAGTGGATTGGTCAGA	TCTGACCAATCCACTGCGTAAGCA
	613	ATGCAGATGAACAAATCGCCGAAT	ATTCGGCGATTTGTTTCATCTGCAT
	614	GCAATTCTGGGCCATGTATTCGTC	GACGAATACATGGCCGAGAATTGC
	615	AGGGTTCCTTACGCGTCGACATGG	CCATGTGCGACGCGTAAGGAACCCT
30	616	GTGGAGCTAATCGCGAGCCTCAGA	TCTGAGGCTCGCGATTAGCTCCAC
	617	TCGTAGTCTACCCGGCAATGATCC	GGATCATTGCCGGTGAGACTACGA
	618	TTATAGCAGTGCGCCAATGCTTCG	CGAAGCATTGGCGCACTGCTATAA
	619	CGAACAGTGCTGTCCGTGCTCAA	TTGAGCGACGGACAGCACTGTTCCG
	620	TCCGCGTGGACTGTTAGACGCTAT	ATAGCGTCTAACAGTCCACGCGGA
35	621	CATTAGCCCGCTGTGCGTAACTGT	ACAGTTACCGACAGCGGGCTAATG
	622	GGAAAGAACTCAGACGCGCAATG	CATTGCGCGTCTGAGTTTCTTTCC
	623	CGACTCGCTGGACAGGAGAATCGT	ACGATTCTCCTGTCCAGCGAGTCG
	624	CATGATCCTCTGTTTACCCGCGG	CCGCGGGTGAAACAGAGGATCATG
	625	GGCGTAGCGCTCTAAAAGCTTCGG	CCGAAGCTTTTAGAGCGCTACGCC
40	626	AGTGATGCCATCAGGCCCGTATAC	GTATACGGGCCTGATGGCATCACT
	627	TATGGAAAGGGCAACAGCGCTATC	GATAGCGCTGTTGCCCTTTCCATA

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628	CTGTGGTTGATGGAGGATCCACAC	GTGTGGATCCTCCATCAACCACAG
629	ACTCGCTGGAATTTGCGCTGACAC	GTGTCAGCGCAAATTCAGCGAGT
630	CAGGCCCCGAACCACGCGGTTACAG	CTGTAACCGCGTGGTTCGGGCCTG
631	GGCGCAATGGGCGCATAAATACTA	TAGTATTTATGCGCCCATTCGCGCC
632	GGTCAATTCGCGCTACATGCCCTA	TAGGGCATGTAGCGCGAATTGACC
633	GATGGTGGACTGGAGCCCTTCCGC	GCGGAAGGGCTCCAGTCCACCATC
634	CCGCGCATAGCGCAATAGGGGAGA	TCTCCCCTATTGCGCTATGCGCGG
635	TCTTCTGGCTGTCCGGCACCCGAA	TTCGGGTGCCGGACAGCCAGAAGA
636	GCGTTCGCAATTCACGGGCCCTTA	TAAGGGCCCGTGAATTGCGAACGC
637	TCGTTTCGGCCTTGAGAGTATCG	CGATACTCTCAAGGCCGAAACGA
638	AGGTGCAAGTGCAAGGCGAGAGGC	GCCTCTCGCCTTGCACTTGACCT
639	CGCCAGTTTCGATGGCTGACGTTT	AAACGTCAGCCATCGAACTGGCG
640	GCTTTACCGCCGATCCAGATATC	GATATCTGGGATCGGCGGTAAAGC
641	GTGCTTGACGAAGAGGCGAAATGT	ACATTTGCGCTCTTCGTCAAGCAC
642	CAGTCCGTGCGCTTCATGTCCTCA	TGAGGACATGAAGCGCACGGACTG
643	TACGCGTAAGAGCCTACCCTCGCG	CGCGAGGGTAGGCTCTTACGCGTA
644	GGCGAGTCTTGTGGGGACATGTGT	ACACATGTCCCCACAAGACTCGCC
645	CCAAAGCGAAGCGAGCGTGTCTAT	ATAGACACGCTCGCTTCGCTTTGG
646	GCCGTAGGTTGCTCTTCACCGAAC	GTTTCGGTGAAGAGCAACCTACGGC
647	AAATCCGCGATGTGCCGTGAGGCT	AGCCTCACGGCACATCGCGGATTT
648	GGCTTCGCACCCGTACCAATTTAG	CTAAATTGGTACGGGTGCGAAGCC
649	TGTAGAGTCCCACGTAGCCGGCAT	ATGCCGGCTACGTGGGACTCTACA
650	CACTAGTCTGGGGCAAGGTGCATT	AATGCACCTTGCCCCAGACTAGTG
651	TGTACTCGGCAGGCGCAATAGATT	AATCTATTGCGCCTGCCGAGTACA
652	AACGGGTATCGGAAGCGTAAAAGC	GCTTTTACGCTTCGATACCCGTT
653	CGGACTGCCCGTTTGCAAGTTGAG	CTCAACTTGCAAACGGGCAGTCCG
654	ATCGTTTCAGCACTGGAGCCCCTAA	TTACGGGCTCCAGTGCTGAACGAT
655	ATGCATCGAACTAGTCGTGACGGC	GCCGTCACGACTAGTTCGATGCAT
656	TTCCAGGCATTAAGGAGAGGGAGC	GCTCCCTCTCCTTAATGCCTGGAA
657	GTGCGACATCTACTCCACGATCCC	GGGATCGTGGAGTAGATGTCGCAC
658	CTCATCGTCCTAACACGAGAGCCC	GGGCTCTCGTGTTAGGACGATGAG
659	AATGGCACTTCGGCGGTGATGCAA	TTGCATCACCGCCGAAGTGCCATT
660	CCGTGGGAGGGAATCCAACCGAGG	CCTCGGTTGGATTCCCTCCCACGG
661	AAATTCTCGTTGGTGACGGCTCAT	ATGAGCCGTACCAACGAGAATTT
662	TTGCTCTTATCCTTGTCCTGGGCG	CGCCCAGGACAAGGATAAGAGCAA
663	TTAAGGATCAGGCGGAGCTTGACG	CTGCAAGCTCCGCCTGATCCTTAA
664	CGCGACTAAGGTGCTGCAACTCGA	TCGAGTTGCAGCACCTTAGTCGCG
665	GCTCGATTTACGGCCCGTTGTTC	GAACAACGGGCCGTGAAATCGAGC
666	AGCAGAGTGCGTTGCAGAGGCTAA	TTAGCCTCTGCAACGCACTCTGCT
667	TGGAGGTGAGGACGACGTGCACTA	TAGTGACGTCGTCTCACCTCCA
668	AACCGTTTAGGGTACATTCGCGGT	ACCGCGAATGTACCCTAAACGGTT

	669	TATGATCGCTCGGCTCACAGTTTG	CAAACGTGAGCCGAGCGATCATA
	670	GACTTTTTGCGGAAACGTCATGGT	ACCATGACGTTTCCGCAAAAAGTC
	671	TGTCGGTTATTCCACCTGCAAGGA	TCCTTGCAGGTGGAATAACCGACA
	672	CTATGGTTTGCACCTGCGCCGTCGA	TCGACGGCGCAGTGCAAACCATAG
5	673	AGCAGGGAAATTCAATCGTTCGCA	TGCGAACGATTGAATTTCCCTGCT
	674	CCTAACCGAGCGCTTAGCATTTC	GGAAATGCTAAGCGCTCGGTTAGG
	675	CCCGACCCTAACTCGCATTGAATA	TATTCATGCGAGTTAGGGTCGGG
	676	TTGCTTAATGGTGACGCCACGGAT	ATCCGTGGCGTCACCATTAAGCAA
	677	GATGCTCGCCGTGTTTAGTTCACG	CGTGAATAAACACGGCGAGCATC
10	678	TCGGATGACGAGTTTCCATGACGG	CCGTCATGGAACTCGTCATCCGA
	679	ATGCGGTCTACTTCTCGATCGGG	CCCGATCGAGAAAGTAGACCGCAT
	680	TTGCGAGGCTAAGCACACGGTAAA	TTTACCGTGTGCTTAGCCTCGCAA
	681	AACTTAATTACCGCCTCTGGCGCC	GGCGCCAGAGGCGGTAATTAAGTT
	682	GTGACCGCGAACTTGTTCCGACAG	CTGTGGAACAAGTTCGCGGTAC
15	683	TGCGGATTACCGATTCTGCTCTTAA	TTAAGAGCGAATCGGTAATCCGCA
	684	TGATAGGGGGCCACGTTGATCAGA	TCTGATCAACGTGGCCCCCTATCA
	685	TCGCTCCGTAGCGATTTCATCGTAG	CTACGATGAATCGCTACGGAGCGA
	686	TGTCAGCTGGTAGCCTCCGTTTGA	TCAAACGAGGCTACCAGCTGACA
	687	AGCGTCGCATGACGCTTACGGCAC	GTGCCGTAAGCGTCATGCGACGCT
20	14	AGACGCACCGCAACAGGCTGTCAA	TTGACAGCCTGTTGCGGTGCGTCT
	15	CGTGTAGGGGTCCCGTGCTGTCAA	TTGACAGCACGGGACCCCTACACG
	690	GTCGCATTCTGCACTGGCTTCGCC	GGCGAAGCCAGTGCAGAATGCGAC
	691	TGATTAGGTGCGGTCCCGTAGTCC	GGACTACGGGACCGCACCTAATCA
	692	AAGGGACCTTGGGTGACGGCGAGA	TCTCGCCGTACCCAAGGTCCCTT
25	693	TCAAATGGCCACCGCGTGTCATTC	GAATGACACGCGGTGGCCATTGTA
	694	CTCCGACGACCAATAAATAGCCGC	GCGGCTATTTATTGGTCGTCGGAG
	695	GGCTATTCCCGTAGAGAGCGTCCA	TGGACGCTCTCTACGGGAATAGCC
	696	TGGATAACCTCTCGGTCCATCCAC	GTGGATGGACCGAGAGGTTATCCA
	697	GACCGCTGTACGGGAGTGTGCCTT	AAGGCACACTCCCGTACAGCGGTC
30	698	GCCACAGAGTTTTAGCAGGGACCC	GGGTCCCTGCTAAAACTCTGTGGC
	699	CCCACGCTTTCGACCACTGACCT	AGGTCAGTGGTCGAAAGCGTGGG
	700	CATTGACACAATGCGGGGACTGAT	ATCAGTCCCCGCATTGTGTCAATG
	701	AGCCACTCGACAGGGTTCCAAAGC	GCTTTGGAACCCTGTGAGTGGCT
	702	CAGGATGAGCAAAGCGACTCTCCA	TGGAGAGTCGCTTTGCTCATCCTG
35	703	CAAGGTATGGTCTGGGGCCTAAGC	GCTTAGGCCCCAGACCATACCTTG
	704	GGTGTTCCGGCCTAAACTCTTTCGG	CCGAAAGAGTTTAGGCCGAACACC
	705	TTTAGTCGGACCCTGTGGCAATTC	GAATTGCCACAGGGTCCGACTAAA
	706	CACACGTTTCCGACCAGCCTGAAC	GTTTCAGGCTGGTCGAAACGTGTG
	707	CTGGACGAACTGGCTTCCTCGTAC	GTACGAGGAAGCCAGTTCGTCCAG
40	708	TTCACAATCCGCCGAAACTGACC	GGTCAGTTTTCGGCGGATTGTGAA
	709	AACAGGATATCCGCGATCACGACA	TGTCGTGATCGCGGATATCCTGTT

	710	TACGTCGGATCCATTGCGCCGAGT	ACTCGGCGCAATGGATCCGACGTA
	711	CATGGATCTCTCGGTTTGATCGCC	GGCGATCAAACCGAGAGATCCATG
	712	AGCCAGGCGCGTATATACGCTCGG	CCGAGCGTATATACGCGCCTGGCT
	713	ATTTGGCACGTGTCTGTCGTCATGTT	AACATGGCACGACACGTGCCAAAT
5	714	CCGCGTTGCACCACTTTGAGGTGC	GCACCTCAAAGTGGTGAACGCGG
	715	TTGGACGTGACAAGCATGCGGCTC	GAGCGCCATGCTTGTACGTCCAA
	716	CTGAATCGCGCAAGTAAATGGGGG	CCCCATTTACTTGCGCGATTGAG
	717	GATAAGGTCCACCAGATTGCGCGC	GCGCGCAATCTGGTGGACCTTATC
	718	CTAACAATTGCCAACCGGGACGGC	GCCGTCCCGGTTGGCAATTGTTAG
10	719	GGTAACCTGGGTGCTTGACAGGTTA	TAACCTGCAAGCACCCAGGTTACC
	720	ATCGGAGCCACCATTGCGATTGGG	CCCAATGCGAATGGTGGCTCCGAT
	721	GTGAACTGGCTTGCCCCAGGATTA	TAATCCTGGGGCAAGCCAGTTCAC
	722	AGGCGATAGCATGGTCCCATATGA	TCATATGGGACCATGCTATCGCCT
	723	AACGGTATCGTGCTAATGCACGA	TCGTGCATTAGCCACGATACCGTT
15	724	AGTAGTGGTCTCCAGATCGGCAA	TTGCCGATCTGGAGGACCACTACT
	725	CCGTTGAATTGGACGGGAGGTTAG	CTAACCTCCCGTCCAATTCAACGG
	726	GCATAAGTGCGGCATCGCGAAGGG	CCCTTCGCGATGCCGCACTTATGC
	727	CGACAAGATGCAGCTGCTACATGC	GCATGTAGCAGCTGCATCTTGTCG
	728	TCGCAGTGATTCCCGACCGATAAG	CTTATCGGTCGGGAATCACTGCGA
20	729	CAAGGCGAGTCCACTCGAGGGGAC	GTCCCCTCGAGTGGACTCGCCTTG
	730	GCAACTTGACGCGCATAAGTGGCC	GGCCACTTATGCCGTGCAAGTTGC
	731	TCCGAGCTTGACGTTGCGGACGTC	GACGTCGCGAACGTCAAGCTCGGA
	732	AGCGCTGGGCTGTGCTGCCATCTC	GAGATGGCAGCACAGCCCAGCGCT
	733	TTCATGTCGCTGAGTAACCCTCGC	GCGAGGGTACTCAGCGACATGAA
25	734	CGAACCGCTAATGCCCATTTGTCAG	CTGACAATGGGCATTAGCGGTTG
	735	CACGGAAGGTGGGACAAATCGCCG	CGGCGATTTGTCCACCTTCCGTG
	736	CACAGATGGAGACAAACGCGCCTT	AAGGCGCGTTTGTCTCCATCTGTG
	737	TTTTCGCAACTCGCTCCATAACCC	GGGTTATGGAGCGAGTTGCGAAAA
	738	ACGTTACGTTTCCGGCGCCTCTAA	TTAGAGGCGCCGAAACGTAACGT
30	739	TATCGGATTGCGTGGGTTTCAATC	GATTGAAACCCACGCAATCCGATA
	740	CTTCCACAATTGTCTGCGACGCAC	GTGCGTCGACAGACAATTGTGGAAG
	741	TGCACAAAGGTATGGCTGTCCGGC	GCCGGACAGCCATACCTTTGTGCA
	742	TCCGATGCCAGTCCCATCTTAAGA	TCTTAAGATGGGACTGGCATCGGA
	743	CTGAAACCGTGCGAATCGAGGTGA	TCACCTCGATTGCGACGGTTTCAG
35	744	CGGTGTTCCGCGTGTGAAAAAAT	ATTTTTTCGACACGCGGAACACCG
	745	TCTAGCAGGCCTTTTGAATCGCCA	TGGCGATTCAAAGGCCTGCTAGA
	746	GAGTCACCTCTGAGACGGACGCCA	TGGCGTCCGTCTCAGAGGTGACTC
	747	TCTTCTGTATCCTGCAGCAGCAT	ATGCTGCTGCAGGATGACAGAAGA
	748	GCGGATGAAACCTGAAAGGGGCCT	AGGCCCTTTTCAAGTTTCATCCGC
40	749	GGGGCCCCAACTGGTATCAAGCC	GGCTTGATACCAGTTTGGGGCCCC
	750	GCATTGGCTTCGGAATTCTCTACA	TGTAGGAGAATCCGAAGCCAATGC

	751	AGGCGGCCCAACTGTGAGGTCTTG	CAAGACCTCACAGTTGGGCCGCCT
	752	ACACCATGTGCTCCGCGCTGCAGT	ACTGCAGCGCGGAGCACATGGTGT
	753	ACGATGAACATGAATCGGGAGTCG	CGACTCCCGATTTCATGTTTCATCGT
	754	CTGCATCCCTGTAGCAGCGCTCCG	CGGAGCGCTGCTACAGGGATGCAG
5	755	GTGCCGTATTTTCGACCTGTGCGTT	AACGCACAGGTCGAAATACGGCAC
	756	GCAGTGCGCACTTCAGTTCAAAAG	CTTTTGAAGTGAAGTGCGCACTGC
	757	GCGATTTTAAGCGATGCCTTGACG	CGTCAAGGCATCGCTTAAAATCGC
	758	TAGGTGACCTAGGCTTGCTTGCGG	CCGCAAGCAAGCCTAGGTCACCTA
	759	CTGGATACCTTGCTGTGCGGCGC	GCGCCGCACAGGCAAGGTATCCAG
10	760	CCCCTTACGGCTCGTCGTCTATGC	GCATAGACGACGAGCCGTAAGGGG
	761	GCGCTTGCCCGATGCGATGCATTA	TAATGCATCGCATCGGGCAAGCGC
	762	TTTCTGTAAGCGGCCTGGGGTTCA	TGAACCCAGGCCGCTTACAGAAA
	763	GGCTGAGGTGAGCGGTAAGGATGA	TCATCCTTACCGCTCACCTCAGCC
	764	TCTTGGCCTCCCCGATCTAATTTG	CAAATTAGATCGGGGAGGCCAAGA
15	765	GGAGGTAACGCCGTGTACGTAGGA	TCCTACGTACACGGCGTTACCTCC
	766	GTAATCCATTTGTGGCTGCGTCAA	TTGACGCAGCCACAAATGGATTAC
	767	CAAACCCATTCCAGCAGACGCCTG	CAGGCGTCTGCTGGAATGGGTTTG
	768	TAGGAGGAATTTGGCATGCGGGCG	CGCCCGCATGCCAAATTCCTCCTA
	769	ATAGGTAGGATGTGCCCGCGTTG	CAACGCCGGGCACATCCTACCTAT
20	770	GCAAGTGCTTAGCTCGTCAGCCTC	GAGGCTGACGAGCTAAGCACTTGC
	771	CTGGCTGTGTGCGCATCTCGTTAAC	GTTAACGAGATGCGACACAGCCAG
	772	CTAACGTCGTCTCGCGCAATCACT	AGTGATTGCGCGAGACGACGTTAG
	773	TTTTCATAAACGTTGTCCCCGAGC	GCTCGGGGACAACGTTTATGAAAA
	774	AGCAGGAGGACGAACCTCCGCTCC	GGAGCGGAGGTTCTGCTCCTGCT
25	775	TTCAAGCACCATCGTGCAATCAA	TTGGATTGCACGATGGTGCTTGAA
	776	AGCGTCGCCAGTGATCGCTAGTGG	CCACTAGCGATCACTGGCGACGCT
	777	TACATTCCTGCCTCCGTGGGCTT	AAGCCACGGAGGCAGGGAATGTA
	778	CGCTTCGCGTATTTCAGTAGCGGTT	AACCGCTACTGAATACGCGAAGCG
	779	TCGGACGCGTCGACACTCATTATA	TATAATGAGTGTGACGCGTCCGA
30	780	TCTGAGCAGGCCAGCGCTCCAGCT	AGCTGGAGCGCTGGCCTGCTCAGA
	781	TTGAATTGCCAAGCCCTGAAAGCC	GGCTTTCAGGGCTTGGCAATTCAA
	782	AGTTTTCGCCTTGATGCGTCGGTG	CACCGACGCATCAAGGCGAAAAT
	783	GTTTCATAGGCCACGCGTGCTAAA	TTTAGCACGCGTGGCCTATGAAAC
	18	CATCGCTGCAAGTACCGCACTCAA	TTGAGTGCGGTACTTGACGCGATG



TABLE 4

Seq. ID No.	Decoder Sequence (5'-3') + 5' T	Probe Sequence (5'-3') + 5' T
17	TTTCGCCGTCGTGTAGGCTTTTCAA	TTTGAAAAGCCTACACGACGGCGAA
18	TGTTCCCAGTGAAGCTGCGATCTGG	TCCAGATCGCAGCTTCACTGGGAAC
19	TTACTTGGCATGGAATCCCTTACGC	TGCGTAAGGGATTCCATGCCAAGTA
20	TACTAGCATATTTCAAGGACCGGC	TGCCGGTGCCCTGAAATATGCTAGT
21	TGAACGGTCAATGAACCCGCTGTGA	TTACAGCGGGTTCATTGACCGTTC
22	TGCGGCCTTGTTCAATATGAATCG	TCGATTCATATTGAACCAAGGCCGC
23	TGATCGTTAGAGGGACCTTGCCCGA	TTCCGGCAAGGTCCCTCTAACGATC
24	TTGGACCTAGTCCGGCAGTGACGAA	TTTCGTCACTGCCGGACTAGGTCCA
25	TATAAACTACCCAGGACGGGCGGAA	TTTCCGCCCGTCCTGGGTAGTTTAT
26	TCATCGGTTGCGGCCAATCCAGATA	TTATCTGGATTGGCGCGAACCGATG
27	TGTCGGGCATAGAGCCGACCACCCT	TAGGGTGGTCGGCTCTATGCCCGAC
28	TCTTGGGTCATGATTACCGTGCTA	TTAGCACGGTGAATCATGACCCAAG
29	TTGCCTAACGTGCTAATCAGCAGCG	TCGCTGCTGATTAGCACGTTAGGCA
30	TCGCATGTTGGAGCATATGCCCTGA	TTCAGGGCATATGCTCCAACATGCG
31	TAGCCACTGCATCAGTGCTGTTCAA	TTTGAACAGCACTGATGCAGTGGCT
32	TGGTTGTTTTGAGGCGTCCCACACT	TAGTGTGGGACGCCTCAAAACAACC
33	TTCGACCAAGAGCAAGGGCGGACCA	TTGGTCCGCCCTTGCTCTTGGTCGA
34	TGACATCGCTATTGCGCATGGATCA	TTGATCCATGCGCAATAGCGATGTC
35	TGAAATACGAAGTCTGCGGGAGTCG	TCGACTCCCGCAGACTTCGTATTTTC
36	TTGTCATGAATGATTGATCGCGCGA	TTGCGCGCATCAATCATTATGACA
37	TATATCGGGATTTCGTTCCCGGTGAA	TTTCACCGGGAACGAATCCCGATAT
38	TGCGAGCGTACCGAAGGGCCTAGAA	TTTCTAGGCCCTTCGGTACGCTCGC
39	TTTACCGGCAGCGGACTTCCGAATT	TAATTCGGAAGTCCGCTGCCGGTAA
40	TGTAATCGAGAGCTGCGCGCCGTCT	TAGACGGCGCGCAGCTCTCGATTAC
41	TCCTGTTAGCGTAGGCGAGTCGATC	TGATCGACTCGCCTACGCTAACAGG
42	TTAGCGGACCGGCAGAATGAGTTCC	TGGAACTCATTCTGCCGGTCCGCTA
43	TGGTACATGCACTACGCGCACTCGG	TCCGAGTGC GCGTAGTGCATGTACC
44	TAATTCATCTCGGACTCCCGCGGTA	TTACCGCGGGAGTCCGAGATGAATT
45	TGCCAAATCTGGATTGGCAGGAATG	TCATTCTGCCAATCCAGATTITGGC
46	TTGCATTTTCGGTTGAGGCACATCC	TGGATGTGCCTCAACCGAAAATGCA
47	TCCGCTCAATTCACCATGCTTCGCT	TAGCGAAGCATGGTGAATTGAGCGG
48	TCTCGGAAAGGTGCAACTTTGGTGT	TACACCAAAGTTGCACCTTTCCGAG
49	TAATTCGACCAGCAGAACGTCCCAT	TATGGGACGTTCTGCTGGTCAATT
50	TGCCAGAGTCTCAACCTCACGGGAT	TATCCCGTGAGGTTGAGACTCTGGC
51	TCCAACAAC TGGAACGGGAACCCGC	TGCGGGTTC CGGTTCCAGTTGTTGG
52	TGAGAACTGATCGCTGAGGGGCATG	TCATGCCCTCAGCGATCAGTTCTC
53	TGGCACACTAGACTTGTGGCACCGA	TTCCGGTGCCACAAGTCTAGTGTGCC

54	TTCACATCCAAATATGGTCCGCGAA	TTTCGCGGACCATATTTGGATGTGA
55	TGTCTGCCGGTGTGACCGCTTCATT	TAATGAAGCGGTCACACCGGCAGAC
56	TCATCGCAGAGCATAAACACCCTCA	TTGAGGGTGTTTATGCTCTGCGATG
57	TGTTGGTATCTATGGCAGAGGCGGA	TTCCGCCTCTGCCATAGATACCAAC
58	TACGAGGTGCCGCTGAGGTTCCATT	TAATGGAACCTCAGCGGCACCTCGT
59	TGGAATGAGTGGACCCAGGCACATT	TAATGTGCCTGGGTCCACTCATTCC
60	TTGTCAATATGCGTCCGTGTCGTCT	TAGACGACACGGACGCATATTGACA
61	TTGATGAGCCTCAGGGTACGAGGCA	TTGCCTCGTACCCTGAGGCTCATCA
62	TCACCGCGGTGTTCTACAGAAATGA	TTCAATTCTGTAGGAACACCGCGGTG
63	TTTGTTGCCAATGGTGTCCGCTCGG	TCCGAGCGGACACCATTGGCAACAA
64	TTTAACCTGCGTCTGCCCTTTCTCT	TAGGAAAGGGGCAGACGCAGGTTAA
65	TAGGCGCGTTCCTGCCTTAGTGACG	TCGTCACTAAGGCAGGAACGCGCCT
66	TTAGGGCGATGGCACGAAGCTTCAA	TTTGAAGCTTCGTGCCATCGCCCTA
67	TTGCATAGAGCCAAAGTCGGCGATG	TCATCGCCGACTTTGGCTCTATGCA
68	TTTGAGAGGCAGGTGGCCACACGGA	TTCCGTGTGGCCACCTGCCTCTCAA
69	TTCCGCATTGTGAGAAAAACGAGC	TGCTCGTTTTTCTCACAATGCGGA
70	TGGCGGTTTCCGTAGCTATAGGTGC	TGCACCTATAGCTACGGAACCGCC
71	TGGTGAAAATTCGTAGCCACGGGC	TGCCCGTGGCTACGAAATTTTACC
72	TCCGACGGAGGATGAAGACAATCAC	TGTGATTGTCTTCATCCTCCGTCCG
73	TCCAGTTTGCCCAATTCGCCAAAA	TTTTTGCGCAATTGGGCCAACTGG
74	TGGATCTATTAGGCCGTGCGCACAG	TCTGTGCGCACGGCCTAATAGATCC
75	TCGGATGTCACCGTTTGGACTTTCA	TTGAAAGTCCAAACGGTGACATCCG
76	TATCGCAAAATCCTGCTCGTCCCTAA	TTTAGGGACGAGCAGGATTTGCGAT
77	TCAGGGCATGCAATAATCGAGGTTT	TGAACCTCGATTATTGCATGCCCTG
78	TCATGCGTTGATATATGGGCCCAAG	TCTTGGGCCCATATATCAACGCATG
79	TCAGCTGCAGCTTGTGACCAACCAC	TGTGGTTGGTCACAAGCTGCAGCTG
80	TTTGTATGTCTGCCGACCGGCGACC	TGGTCGCCGGTCGGCAGACATACAA
81	TGATGGCGCCCGTTGATAGGTATGG	TCCATACCTATCAACGGGCGCCATC
82	TATGAGAATCGCCGGCAATCTGCTA	TTAGCAGATTGCCGGCGATTCTCAT
83	TATTTGCACTGACCGCAGGCTCGTG	TCACGAGCCTGCGGTCAGTGCAAT
84	TCAGGGAGAACGGTTAAGTTCCCGT	TACGGGAACCTTAACCGTTCTCCCTG
85	TAGGCCGGCGATCGAGGAGTTTGGT	TACCAAACTCCTCGATCGCCGGCCT
86	TACACGGTGGTCTCTGATAGCGACC	TGGTCGCTATCAGAGACCACCGTGT
87	TGTGCAACGCCGAGGACTTCCATCA	TTGATGGAAGTCTCGGCGTTGCAC
88	TTCCGTGCCTGATAGCCATTCCGAT	TATCGGAATGGCTATCAGGCACCGA
89	TTGAAATACCACACAGCCAATTGGC	TGCCAATTGGCTGTGTGGTATTTCA
90	TGCATCGTGTACATGACTGCCGCGA	TTCCGCGCAGTCATGTACACGATGC
91	TCAGTGTTCTAACGGCGCGCGTGAA	TTTACGCGCGCCGTTAGAACACTG
92	TCGCTTGCAACGTTGCACCTACTCT	TAGAGTAGGTGCAACGTTGCAAGCG
93	TCGAAAACTAGTGGGCTCGCCGCG	TCGCGGCGAGCCCACTAGTTTTTCG
94	TCTTTCAGGGGAACTGCCGGAGTCG	TCGACTCCGGCAGTTCCTTCAAAG

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95	TTTGTGGCCTTCTTGTAAGGCACG	TCGTGCCTTTACAAGAAGGCCACAA
96	TTCCACGAACGGCGACCCGTTGTCT	TAGACAACGGGTCGCCGTTCTGGA
97	TCGACCTTGACACGAAACCTAACGAG	TCTCGTTAGGTTTCGTGCAAGGTCG
98	TGTGCAGCTTCACGAGCCAGCCTGA	TTCAGGCTGGCTCGTGAAGCTGCAC
99	TCGCTTTCGTGCGAATAGACGATGA	TTCATCGTCTATTGCGACGAAAGCG
100	TTGCGCTTACAGGCTCCTAGTGGTC	TGACCACTAGGAGCCTGTAAGCGCA
101	TCACGCGCTTAGTCGCGATCGCATA	TTATGCGATCGCGACTAAGCGCGTG
102	TCGGAGGGAGGGAGCTAGCCTTCGA	TTGGAAGGCTAGCTCCCTCCCTCCG
103	TGCATCCGGCCTGTTGATGACGCCT	TAGGCGTCATCAACAGGCCGGATGC
104	TAGGCCAATCGATCTTATTGCCGAG	TCTCGGCAATAAGATCGATTGGCCT
105	TCCTTCCAATGATTGCATACGCCCA	TTGGGCGTATGCAATCATTGGAAGG
106	TAACACTTGATCAGGCGGGTCGTCT	TAGACGACCCGCTGATCAAGTGTT
107	TTGGAATCAAGGCCGTAAAGGACAG	TCTGTCTTTACGGCCTTGATTCCA
108	TGCTCCCGTAACCTGTCCACCAGTG	TCACTGGTGGACAGGTTACGGGAGC
109	TAGTGGTGAATGGCCGCTACCCTGA	TTCAGGGTAGCGGCCATTCACTACT
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111	TCAGCGCTCCAGAATTGACAGCAAT	TATTGCTGTCAATTCTGGAGCGCTG
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3	TAACGCGTGGGGAATGGGACATCAA	TTTGATGTCCCATTTCCACGCGTT
114	TCACGAGATACGGCGTAAGGGTGG	TCCACCCTTACGCCGGTATCTCGTG
115	TCTACGGCAAACGTGTGGAATGGGT	TACCCATTCCACACGTTTGCCGTAG
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117	TAATCGACCTCCGCACACATTGCA	TTGCGAATGTGTGCGGAGGTCGATT
118	TGAGTCAGCATGGCGGCGGAGATTC	TGAATCTCCGCCGCCATGCTGACTC
119	TAGATAAAGACGCTGGCAACACGGG	TCCCGTGTTGCCAGCGTCTTTATCT
120	TGGTACCTCAACGCGAACCCTTGT	TACAAGTGGTTGCGGTTGAGGTACC
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123	TATCGGTCTCACGCAGGGTTGGATA	TTATCCAACCCTGCGTGAGACCGAT
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125	TCGGTGCTGTTGCAAAAGCCTGTAG	TCTACAGGCTTTTGCAACAGCACCG
126	TTGATGAAAGTTTGCGGCAGGACAC	TGTGTCCTGCCGCAAACCTTCATCA
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128	TAACATTGCGCGGTCCACCAGGGTT	TAACCCTGGTGGACCGCGCAATGTT
129	TGGGCAGTTAGAGAGGGCCAGAAGT	TACTTCTGGCCCTCTCTAACTGCC
130	TTGAGCTGGTCCCCGTGAACGTGT	TACACGTTACGGGGACCAGCTCGA
131	TGCTTTGGGGGCCGCTTAGTGAAAA	TTTTTCACTAAGCGGCCCCCAAGAC
132	TACTGTTGGCTTGCTCTCATGTCCA	TTGGACATGAGAGCAAGCCAACAGT
133	TAGGACCATTGGAAGGCGAAGATA	TTATCTTCGCCTTCCGAATGGTCCT
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	138	TACCTGATCGTTCCCCTATTGGGAA	TTTCCCAATAGGGGAACGATCAGGT
	139	TGGAACAGAGGCGAGGGGACTGAGC	TGCTCAGTCCCCTCGCCTCTGTTCC
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	142	TCTGACGGTTTTTCATTGCGCGTGCC	TGGCACGCCGAATGAAAACCGTCAG
	143	TTGCGGTGGTTTCATTGGAGCTGGCC	TGGCCAGCTCCAATGAACCACCGCA
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	147	TACAGACGAGCTCCCAACCACATGA	TTCATGTGGTTGGGAGCTCGTCTGT
	148	TGGACGGTTTGTGCTGGATTGTCTG	TCAGACAATCCAGCACAAACCGTCC
	149	TAAAGGCTATTGAGTTGGTTGGGCG	TCGCCCCAACCAACTCAATAGCCTTT
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	157	TCGTGGCGGCCACAGTTTTTGGAGG	TCCTCCAAAACTGTGGCCGCCACG
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	162	TAGCGGAAGTAGTCCTCGGCTCGTC	TGACGAGCCGAGGACTACTTCCGCT
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	166	TTCGTCGAGCAGACGAGATTGCACG	TCGTGCAATCTCGTCTGCTCGACGA
	167	TTCTTTGCCGCGTAACTGACTGCTT	TAAGCAGTCAGTTACGCGGCAAAGA
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	173	TCAAATAACGCCGCTGAATCGGCGT	TACGCCGATTTCAGCGGCGTTATTTG
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	176	TCAGCAGATCCTTCGTAGCGGTCGT	TACGACCGCTACGAAGGATCTGCTG

	177	TGGAACCTGGTGAAGTTGTGCCTCAT	TATGAGGCACAACTCACCAGGTTCC
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	179	TCCCAACGTCACTGAAGCTCACAGT	TACTGTGAGCTTCAGTGACGTTGGG
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	183	TATCCTTTTATCTACTCCGCGGCCGA	TTGCGCCGCGGAGTAGATAAAAGGAT
	184	TAGGCGTGACGCAACAGGATAAACC	TGGTTTATCCTGTTGCTGCACGCCT
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	186	TTTGCCAGGTCCATCGAGACCTGTT	TAACAGGTCTCGATGGACCTGGCAA
	187	TTCCACTATAACTGCGGGTCCGTGT	TACACGGACCCGCGAGTTATAGTGGA
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	197	TGAGCTGACGTCACCATCAGAGGAA	TTTCCTCTGATGGTGACGTCAGCTC
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	203	TAGGCCGTGCAACATCACACAGGAT	TATCCTGTGTGATGTTGCACGGCCT
	204	TGGGCCGTGGTCACGTAATATTGGC	TGCCAATATTACGTGACCACGGCCC
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	207	TGGGGCGGTTACCAAAAAATCCGAT	TATCGGATTTTTTGGTAACCGCCCC
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	5	TATGGCCGTGCTGGGGACAAGTCAA	TTTGACTTGTCGCCAGCACGGCCAT
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	218	TCCCTAATGAGGCCAGTAACCTGCA	TTGCAGGTTACTGGCCTCATTAGGG
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	221	TCCCGCATGCCTGGCGGTATTACAA	TTTGTAATACCGCCAGGCATGCGGG
5	222	TTTAGCAAAGCGGCGCCGTTAGCAA	TTTGCTAACGGCGCCGCTTTGCTAA
	223	TCCCGACACGGGTGACGCTAATAAT	TATTATTACGCTGACCCGTGTCGGG
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	225	TCAAAAGTGTGTTCCCTTGCGCTTG	TCAAGCGCAAGGGAACACACTTTTG
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377	TGGGCCGCAATTCTTGATGTCCATTC	TGAATGGACATCAAGAATGCGGCCC
378	TCCTCGGATGTGGGCTCTCGCCTAG	TCTAGGCGAGAGCCCACATCCGAGG
379	TTAGGCATGTTGGCGTGAGCGCTAT	TATAGCGCTCACGCCAACATGCCTA
380	TCGATACGAACGAGGATGTCCGCCT	TAGGCGGACATCCTCGTTGCTATCG
381	TTACGCCGGTTAGCACGGTGCGCTA	TTAGCGCACCGTGCTAACGGGCGTA

	382	TCATACGATGTCCGGGCCGTGTCGC	TGCGACACGGCCCGGACATCGFATG
	383	TATCCGCAGTTGTATGGCGCGTTAT	TATAACGCGCCATACAACGCGGAT
	384	TGGGTAAGGGACAAAGATGGGATGG	TCCATCCCATCTTTGTCCCTTACCC
5	385	TATTGGAGTGTTTTGGTGAATCCGC	TGCGGATTCACCAAAACACTCCAAT
	386	TGAACCGAGCCAACGTATGGACACG	TCGTGTCCATACGTTGGCTCGGTTT
	387	TGCCGTCAAGCTTAAGGTTTTGGGC	TGCCAAAACCTTAAGCTTGACGGC
	388	TACCTGCTTTTGGGTGGGTGATATG	TCATATCACCCACCCAAAAGCAGGT
	389	TAATCGTGGGCGCAGCAAACGTATA	TTATACGTTTGCTGCGCCACGATT
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	391	TACCCGTCGATGCTTCCTCCTCAGA	TTCTGAGGAGGAAGCATCGACGGGT
	392	TATCCGGGTGGGCGATACAAGAGAT	TATCTCTTGTATCGCCACCCGGAT
	393	TTTCCGCATGAGTCAGCTTTGAAAA	TTTTTCAAAGCTGACTCATGCGGAA
	394	TGCAAAGTCCCACTGGCAAGCCGAT	TATCGGCTTGCCAGTGGGACTTTGC
	395	TCGACCTCGGCTTCATCGTACACAT	TATGTGTACGATGAAGCCGAGGTG
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	397	TCAGATGAAGGATCCACGGCCGGAG	TCTCCGGCCGTGGATCCTTCATCTG
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	399	TTCCGCTAATTTCCAATCAGGGCTC	TGAGCCCTGATTGGAAATTAGCGGA
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	9	TTTCGCTTTGCTGGCTGCACTTCAA	TTTGAAGTGCAGCCACGAAAGCGAA
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	404	TCCGATTACAAATTGACTGACCGCA	TTGCGGTCAGTCAATTGTAAATCGG
	405	TAGACGTACGTGAGCCTCCCGTGTC	TGACACGGGAGGCTCACGTACGTCT
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	408	TTGTTTTTGAATTGACCACACGGGA	TTCCCGTGTGGTCAATTCAAAAACA
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	412	TGAATCACCGAATCACCGACTCGTT	TAACGAGTCGGTGATTCCGGTGATT
	413	TAACCAGCCGCAGTAGCTTACGTG	TCGACGTAAGCTACTGCGGCTGGTT
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	415	TGGTGCTCCGTTTGATCGATCCTCC	TGGAGGATCGATCAAACGGAGCACC
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	419	TTAAAAGTTTCGCGGAGGTCGGGCT	TAGCCCGACCTCCGCGAAACTTTTA
	420	TCGGTCCAGACGAGCTGAGTTCGGC	TGCCGAACTCAGCTCGTCTGGACCG
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	425	TGCATCGGCCGTTTTGACCATATTC	TGAATATGGTCAAAACGGCCGATGC
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	430	TGACATCGGGAGCCGGAACATGAG	TCTCATGTTTCGGGCTCCCGATGTC
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	460	TACCTTGCTCCGCCATGTCTCTCA	TTGAGAGACATGGCGGAGCAAGGGT
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	462	TTGTCTTGCTCCCGAGTACCATTG	TCAATGGTACTCGGGAGCAACGACA
	463	TGTTGTCCGAGACGTTTGTGTCAGC	TGCTGACACAAACGTCTCGGACAAC

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503	TGAGACGCTGTCACTCCGGCAGAAC	TGTTCTGCCGGAGTGACAGCGTCTC
504	TCCACCGGTGCGTTAAGATGCACTT	TAAGTGATCTTAAGCGACCGGTGG

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	624	TCATGATCCTCTGTTTCACCCGCGG	TCCGCGGGTGAAACAGAGGATCATG
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650	TCACTAGTCTGGGGCAAGGTGCATT	TAATGCACCTTGCCCCAGACTAGTG
651	TTGTACTCGGCAGGCGCAATAGATT	TAATCTATTGCGCCTGCCGAGTACA
652	TAACGGGTATCGGAAGCGTAAAGC	TGCTTTTACGCTTCCGATACCCGTT
653	TCGGACTGCCCGTTTGCAAGTTGAG	TCTCAACTTGCAAACGGGCAGTCCG
654	TATCGTTCAGCACTGGAGCCCGTAA	TTTACGGGCTCCAGTGCTGAACGAT
655	TATGCATCGAACTAGTCGTGACGGC	TGCCGTCACGACTAGTTCGATGCAT
656	TTTCCAGGCATTAAGGAGAGGGAGC	TGCTCCCTCTCCTTAATGCCTGGAA
657	TGTGCGACATCTACTCCACGATCCC	TGGGATCGTGGAGTAGATGTCGCAC
658	TCTCATCGTCCTAACACGAGAGCCC	TGGGCTCTCGTGTTAGGACGATGAG
659	TAATGGCACTTCGGCGGTGATGCAA	TTTGCATCACCGCCGAAGTGCCATT
660	TCCGTGGGAGGGAATCCAACCGAGG	TCCTCGGTTGGATTCCCTCCCACGG
661	TAAATTCTCGTTGGTGACGGCTCAT	TATGAGCCGTCACCAACGAGAATTT
662	TTTGCTCTTATCCTTGTCCTGGGCG	TCGCCCAGGACAAGGATAAGAGCAA
663	TTTAAGGATCAGGCGGAGCTTGCA	TCTGCAAGCTCCGCCTGATCCTTAA
664	TCGCGACTAAGGTGCTGCAACTCGA	TTCGAGTTGCAGCACCTTAGTCGCG
665	TGCTCGATTTCACGGCCCGTTGTTT	TGAACAACGGGCGGTGAAATCGAGC
666	TAGCAGAGTGCGTTGCAGAGGCTAA	TTTAGCCTCTGCAACGCACTCTGCT
667	TTGGAGGTGAGGACGACGTGCACTA	TTAGTGACGTCGTCCTCACCTCCA
668	TAACCGTTTAGGGTACATTGCGGGT	TACCGCGAATGTACCCTAAACGGTT



	669	TTATGATCGCTCGGCTCACAGTTTG	TCAAACGTGTGAGCCGAGCGATCATA
	670	TGACTTTTTGCGGAAACGTCATGGT	TACCATGACGTTTCCGCAAAAAGTC
	671	TTGTCGGTTATTCCACCTGCAAGGA	TTCTTGCAGGTGGAATAACCGACA
	672	TCTATGGTTTGCACTGCGCCGTCTGA	TTGACGGCGCAGTGCAAACCATAG
5	673	TAGCAGGGAAATTCAATCGTTCGCA	TTGCGAACGATTGAATTTCCCTGCT
	674	TCCTAACCGAGCGCTTAGCATTTC	TGGAAATGCTAAGCGCTCGGTTAGG
	675	TCCCAGCCCTAACTCGCATTGAATA	TTATTCAATGCGAGTTAGGGTCGGG
	676	TTTGCTTAATGGTGACGCCACGGAT	TATCCGTGGCGTCACCATTAAGCAA
10	677	TGATGCTCGCCGTGTTTAGTTCACG	TCGTGAACTAAACACGGCGAGCATC
	678	TTCGGATGACGAGTTTCCATGACGG	TCCGTCATGGAAACTCGTCATCCGA
	679	TATGCGGTCTACTTTCTCGATCGGG	TCCCGATCGAGAAAGTAGACCGCAT
	680	TTTGCGAGGCTAAGCACACGGTAAA	TTTACCCTGTGCTTAGCCTCGCAA
	681	TAACCTTAATTACCGCCTCTGGCGCC	TGGCGCCAGAGGCGGTAATTAAGTT
	682	TGTGACCGCGAACTTGTTCCGACAG	TCTGTGGAACAAGTTCGCGGTCAC
15	683	TTGCGGATTACCGATTCTGCTCTTAA	TTTAAGAGCGAATCGGTAATCCGCA
	684	TTGATAGGGGGCCACGTTGATCAGA	TTCTGATCAACGTGGCCCCCTATCA
	685	TTGCTCCGTAGCGATTTCATCGTAG	TCTACGATGAATCGCTACGGAGCGA
	686	TTGTCAGCTGGTAGCCTCCGTTTGA	TTCAAACGGAGGCTACCAGCTGACA
	687	TAGCGTCGCATGACGCTTACGGCAC	TGTGCCGTAAGCGTCATGCGACGCT
20	14	TAGACGCACCGCAACAGGCTGTCAA	TTTGACAGCCTGTTGCGGTGCGTCT
	15	TCGTGTAGGGGTCCCCTGCTGTCAA	TTTGACAGCACGGGACCCCTACACG
	690	TGTCGCATTCTGCACTGGCTTCGCC	TGGCGAAGCCAGTGCAGAAATGCGAC
	691	TTGATTAGGTGCGGTCCCCTAGTCC	TGGACTACGGGACCGCACCTAATCA
25	692	TAAGGGACCTTGGGTGACGGCGAGA	TTCTCGCCGTCACCCAAGGTCCCTT
	693	TTCAAATGGCCACCGCGTGTCAATC	TGAATGACACGCGGTGGCCATTTGA
	694	TCTCCGACGACCAATAAATAGCCGC	TGCGGCTATTTATTGGTCGTGCGAG
	695	TGGCTATTCCCGTAGAGAGCGTCCA	TTGGACGCTCTCTACGGGAATAGCC
	696	TTGGATAACCTCTCGGTCCATCCAC	TGTGGATGGACCGAGAGGTTATCCA
	697	TGACCGCTGTACGGGAGTGTGCCTT	TAAGGCACACTCCCGTACAGCGGTC
30	698	TGCCACAGAGTTTTAGCAGGGACCC	TGGGTCCCTGCTAAAACTCTGTGGC
	699	TCCCACGCTTTCGACCACTGACCT	TAGGTCAGTGGTCGGAAAGCGTGGG
	700	TCATTGACACAATGCGGGGACTGAT	TATCAGTCCCCGCATTGTGTCAATG
	701	TAGCCACTCGACAGGGTTCCAAAGC	TGCTTTGGAACCCTGTGAGTGGCT
	702	TCAGGATGAGCAAAGCGACTCTCCA	TTGGAGAGTCGCTTTGCTCATCCTG
35	703	TCAAGGTATGGTCTGGGGCCTAAGC	TGCTTAGGCCCCAGACCATACTTG
	704	TGGTGTTTCGGCCTAAACTCTTTCGG	TCCGAAAGAGTTTAGGCCGAACACC
	705	TTTTAGTCGGACCCTGTGGCAATTC	TGAATTGCCACAGGGTCCGACTAAA
	706	TCACACGTTTCCGACCAGCCTGAAC	TGTTCAAGCTGGTCGGAAACGTGTG
	707	TCTGGACGAACTGGCTTCCTCGTAC	TGTACGAGGAAGCCAGTTTCGTCCAG
40	708	TTTCACAATCCGCCGAAAACCTGACC	TGGTCAGTTTTCGGCGGATTGTGAA
	709	TAACAGGATATCCGCGATCACGACA	TTGTCGTGATCGCGGATATCCTGTT

710	TTACGTCGGATCCATTGCGCCGAGT	TACTCGGCGCAATGGATCCGACGTA
711	TCATGGATCTCTCGGTTTGATCGCC	TGGCGATCAAACCGAGAGATCCATG
712	TAGCCAGGCGCGTATATACGCTCGG	TCCGAGCGTATATACGCGCCTGGCT
713	TATTTGGCACGTGTCTGTGCCATGTT	TAACATGGCACGACACGTGCCAAAT
714	TCCGCGTTGCACCACTTTGAGGTGC	TGCACCTCAAAGTGGTGCAACGCGG
715	TTTGGACGTGACAAGCATGGCGCTC	TGAGCGCCATGCTTGTCACGTCCAA
716	TCTGAATCGCGCAAGTAAATGGGGG	TCCCCCATTTACTTGCGCGATTGAG
717	TGATAAGGTCCACCAGATTGCGCGC	TGCGCGCAATCTGGTGGACCTTATC
718	TCTAACAATTGCCAACCGGGACGGC	TGCCGTCCCGGTTGGCAATTGTTAG
719	TGGTAACCTGGGTGCTTGCAAGTTA	TTAACCTGCAAGCACCCAGGTTACC
720	TATCGGAGCCACCATTGCGATTGGG	TCCAATGCGAATGGTGGCTCCGAT
721	TGTGAACCTGGCTTGCCCCAGGATTA	TTAATCCTGGGGCAAGCCAGTTTAC
722	TAGGCGATAGCATGGTCCCATATGA	TTCATATGGGACCATGCTATCGCCT
723	TAACGGTATCGTGGCTAATGCACGA	TTCTGTGATTAGCCACGATACCGTT
724	TAGTAGTGGTCCTCCAGATCGGCAA	TTTGCCGATCTGGAGGACCACTACT
725	TCCGTTGAATTGGACGGGAGGTTAG	TCTAACCTCCCGTCCAATTCAACGG
726	TGCATAAGTGCGGCATCGCGAAGGG	TCCCTTCGCGATGCCGCACTTATGC
727	TCGACAAGATGCAGCTGCTACATGC	TGCATGTAGCAGCTGCATCTTGTCG
728	TTTCGAGTGATTCCCGACCGATAAG	TCTTATCGGTGCGGAATCACTGCGA
729	TCAAGGCGAGTCCACTCGAGGGGAC	TGTCCCCTCGAGTGGACTCGCCTTG
730	TGCAACTTGCACGGCATAAGTGGCC	TGGCCACTTATGCCGTGCAAGTTGC
731	TTCCGAGCTTGACGTTGCGGACGTC	TGACGTGCGCAACGTCAAGCTCGGA
732	TAGCGCTGGGCTGTGCTGCCATCTC	TGAGATGGCAGCACAGCCCAGCGCT
733	TTTCATGTCGCTGAGTAACCTCGC	TGCGAGGGTTACTCAGCGACATGAA
734	TGAAACCGCTAATGCCATTGTCAG	TCTGACAATGGGCATTAGCGGTTG
735	TCACGGAAGGTGGGACAAATCGCCG	TGCGGCGATTGTCCACCTTCCGTG
736	TCACAGATGGAGACAAACGCGCCTT	TAAGGCGCGTTTGTCTCCATCTGTG
737	TTTTTCGCAACTCGCTCCATAACCC	TGGGTTATGGAGCGAGTTGCGAAAA
738	TACGTTACGTTTCCGGCGCCTCTAA	TTTAGAGGCGCCGAAACGTAACGT
739	TTATCGGATTGCGTGGGTTTCAATC	TGATTGAAACCCACGCAATCCGATA
740	TCTTCCACAATTGTCTGCGACGCAC	TGTGCGTGCAGACAATTGTGGAAG
741	TTGCACAAAGGTATGGCTGTCCGGC	TGCCGGACAGCCATACCTTTGTGCA
742	TTCCGATGCCAGTCCCATTCTAAGA	TTCTTAAGATGGGACTGGCATCGGA
743	TCTGAAACCGTGCGAATCGAGGTGA	TTACCTCGATTGCGACGGTTTCAG
744	TCGGTGTTCCGCGTGTGAAAAAAT	TATTTTTTCGACACGCGGAACACCG
745	TTCTAGCAGGCCTTTTGAATCGCCA	TTGGCGATTCAAAGGCCTGCTAGA
746	TGAGTCACCTCTGAGACGGACGCCA	TTGGCGTCCGTCTCAGAGGTGACTC
747	TTCTTCTGTATCCTGCAGCAGCAT	TATGCTGCTGCAGGATGACAGAAGA
748	TGCGGATGAAACCTGAAAGGGGCCT	TAGGCCCTTTTCAAGTTTTCATCCGC
749	TGGGGCCCCAACTGGTATCAAGCC	TGGCTTGATACAGTTTGGGGCCCC
750	TGCATTGGCTTCGGATTCTCCTACA	TTGTAGGAGAATCCGAAGCCAATGC

	751	TAGGCGGCCCAACTGTGAGGTCTTG	TCAAGACCTCACAGTTGGGCCGCCT
	752	TACACCATGTGCTCCGCGCTGCAGT	TACTGCAGCGCGGAGCACATGGTGT
	753	TACGATGAACATGAATCGGGAGTCG	TCGACTCCCGATTTCATGTTTCATCGT
5	754	TCTGCATCCCTGTAGCAGCGCTCCG	TCGGAGCGCTGCTACAGGGATGCAG
	755	TGTGCCGTATTTGACCTGTGCGTT	TAACGCACAGGTGCAAATACGGCAC
	756	TGCAGTGCGCACTTCAGTTCAAAAG	TCTTTTGAAGTGAAGTGCGCACTGC
	757	TGCGATTTTAAGCGATGCCTTGACG	TCGTCAAGGCATCGCTTAAATCGC
	758	TTAGGTGACCTAGGCTTGCTTGCGG	TCCGCAAGCAAGCCTAGGTCACCTA
10	759	TCTGGATACCTTGCTGTGCGGCGC	TGCGCCGCACAGGCAAGGTATCCAG
	760	TCCCTTACGGCTCGTCGTCTATGC	TGCATAGACGACGAGCCGTAAGGGG
	761	TGCGCTTGCCCGATGCGATGCATTA	TTAATGCATCGCATCGGGCAAGCGC
	762	TTTTCTGTAAGCGGCCTGGGGTTCA	TTGAACCCAGGCCGCTTACAGAAA
	763	TGGCTGAGGTGAGCGGTAAGGATGA	TTTCATCCTTACCGCTCACCTCAGCC
15	764	TTCTTGCCCTCCCGATCTAATTTG	TCAAATTAGATCGGGGAGGCCAAGA
	765	TGGAGGTAACGCCGTGTACGTAGGA	TTCTTACGTACACGGCGTTACCTCC
	766	TGTAATCCATTTGTGGCTGCGTCAA	TTTGACGCAGCCACAAATGGATTAC
	767	TCAAACCCATTCCAGCAGACGCCTG	TCAGGCGTCTGCTGGAATGGGTTTG
	768	TTAGGAGGAATTTGGCATGCGGGCG	TCGCCCCGATGCCAAATTCCTCCTA
20	769	TATAGGTAGGATGTGCCGGCGGTTG	TCAACGCCGGGCACATCCTACCTAT
	770	TGCAAGTGCTTAGCTCGTCAGCCTC	TGAGGCTGACGAGCTAAGCACTTGC
	771	TCTGGCTGTGTGCGATCTCGTTAAC	TGTTAACGAGATGCGACACAGCCAG
	772	TCTAACGTGCTCTCGCGCAATCACT	TAGTGATTGCGCGAGACGACGTTAG
	773	TTTTTCATAAACGTTGTCCCGAGC	TGCTCGGGGACAACGTTTATGAAAA
25	774	TAGCAGGAGGACGAACCTCCGCTCC	TGGAGCGGAGGTTTCGTCTCCTGCT
	775	TTTCAAGCACCATCGTGCAATCCAA	TTTGATTGCACGATGGTGCTTGAA
	776	TAGCGTCGCCAGTGATCGCTAGTGG	TCCACTAGCGATCACTGGCGACGCT
	777	TTACATTCCCTGCCTCCGTGGGCTT	TAAGCCACGGAGGCAGGGAATGTA
	778	TCGCTTCGCGTATTTCAGTAGCGGT	TAACCGCTACTGAATACGCGAAGCG
30	779	TTCGGACGCGTCGACACTCATTATA	TTATAATGAGTGTGACGCGTCCGA
	780	TTCTGAGCAGGCCAGCGCTCCAGCT	TAGCTGGAGCGCTGGCCTGCTCAGA
	781	TTTGAATTGCCAAGCCCTGAAAGCC	TGGCTTTCAGGGCTTGGCAATTCAA
	782	TAGTTTTCGCCTTGATGCGTCGGTG	TCACCGACGCATCAAGGCGAAAAC
	783	TGTTTCATAGGCCACGCGTGCTAAA	TTTGTAGCACGCGTGGCCTATGAAAC
	16	TCATCGCTGCAAGTACCGCACTCAA	TTTGAGTGCGGTACTTGACGCGATG

## CLAIMS

We claim:

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1. An oligonucleotide array comprising an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.

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2. An array according to claim 1, wherein said capture probes are microspheres.

3. An array according to claim 1 or 2 wherein said array is a liquid array.

4. An array according to claim 1, 2 or 3, wherein said array further comprises a solid support.

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5. An array according to claim 1, 2, 3 or 4, wherein said addresses are microspheres and wherein said solid support comprises wells into which said microspheres are individually distributed.

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6. An array according to claim 1, 2, 3 or 4, wherein each address is a different known location, and said wherein each capture probe is attached to one of said known locations.

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7. An array according to claim 1, 2, 3, 4, 5 or 6, wherein said array comprises at least 50 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.

8. An array according to claim 1, 2, 3, 4, 5 or 6 wherein said array comprises at least 100 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.

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9. A kit comprising at least twenty-five nucleic acids selected from the group consisting of sequences substantially complementary to the sequences set forth in Table I, Table II, Table III and Table IV or their complement.

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10. A kit according to claim 9, wherein said kit comprises at least 50 nucleic acids selected from the group consisting of the sequences substantially complementary to the sequences set forth in Table I, Table II, Table III and Table IV or their complement.

11. A kit according to claim 9 or 10, wherein said kit comprises at least 100 nucleic acids selected from the group consisting of the sequences substantially complementary to the sequences set forth in Table I, Table II, Table III and Table IV or their complement.

5 12. A kit according to claim 9, 10 or 11, wherein said nucleic acids further comprise at least a first universal priming sequence.

13. A kit according to claim 9, 10, 11 or 12, wherein said nucleic acid sequence further comprises a sequence substantially complementary to a target domain.

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14. A method of immobilizing a target nucleic acid sequence, said method comprising:

a) attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein said first adapter nucleic acid comprises a sequence substantially complementary to a sequence selected from the sequences set forth in Table I, Table II, Table III, and Table IV;

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b) contacting said modified first target nucleic acid sequence with an array comprising an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4, whereby said target nucleic acid sequence is immobilized.

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15. A method of detecting a target nucleic acid sequence, said method comprising:

a) attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein said first adapter nucleic acid comprises a sequence substantially complementary to a sequence selected from the sequences set forth in Table I, Table II, Table III, and Table IV;

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b) contacting said modified first target nucleic acid sequence with an array comprising: an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4; and

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c) detecting the presence of said modified first target nucleic acid sequence.

16. A method of detecting a target nucleic acid, said method comprising:

a) hybridizing a first adapter probe with a first target nucleic acid, said first adapter probe comprising a first domain that is complementary to said first target nucleic acid and a second domain, said second domain comprising a first sequence substantially complementary to a selected from the group consisting of the sequences set forth in Table I, Table II, Table III and Table IV to form a first hybridization complex;

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- b) contacting said first hybridization complex with an enzyme such that when said first domain of said adapter probe is perfectly complementary with said first target nucleic acid, said first adapter probe is altered resulting in a modified first adapter probe;
- c) contacting said modified first adapter probe with a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that said first capture probe and said modified first adapter probe form a second hybridization complex; and
- d) detecting the presence of said modified first adapter probe as an indication of the presence of said target nucleic acid.

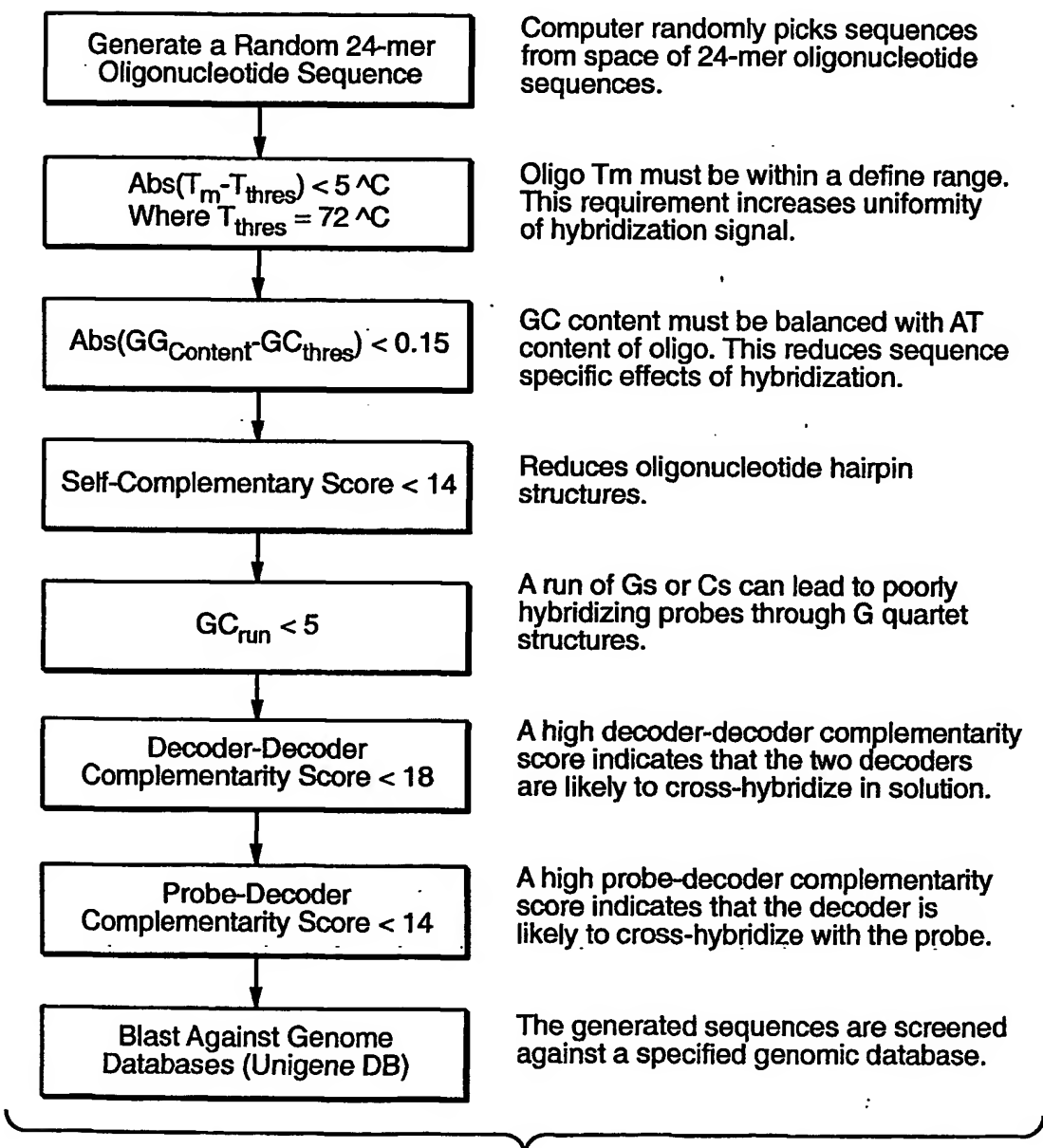
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**Description of algorithm to select “best” oligonucleotide adapter sequences.**

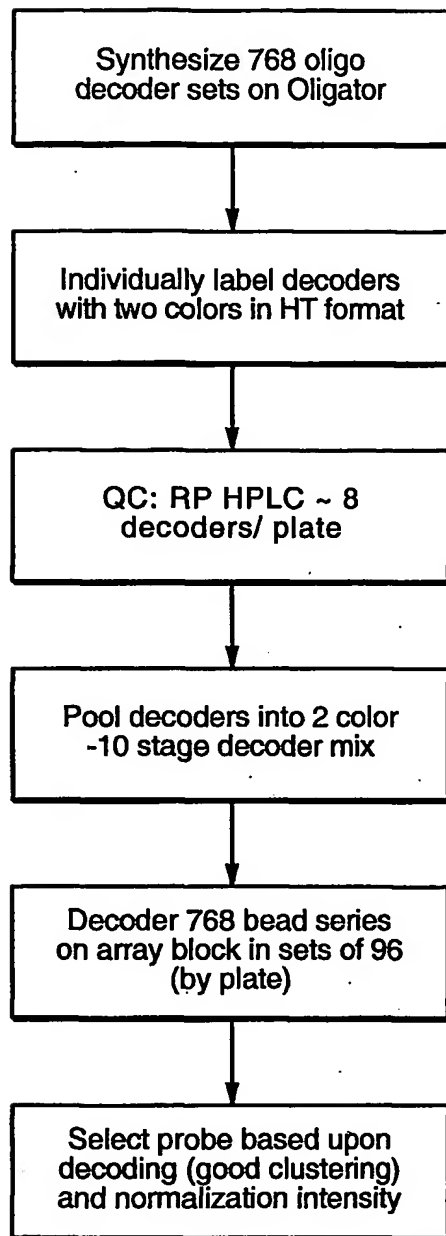
Requirements for good sequences:

- Generates adequate hybridization signal intensity when employed in an experiment.
- Exhibits minimal cross-reactivity with other adapter sequences.
- Unique within the human genome sequence. This requirement can be extended to the genomic sequence of other organisms such as the fruit fly, the mouse, etc.

One method of generating sequences that meet the above requirements is to randomly generate sequences of given lengths and then pass these filters through a set of heuristic acceptance filters. In particular, the 24-mer Illumina Adapter sequences (IllumaCodes) were chosen as follows.

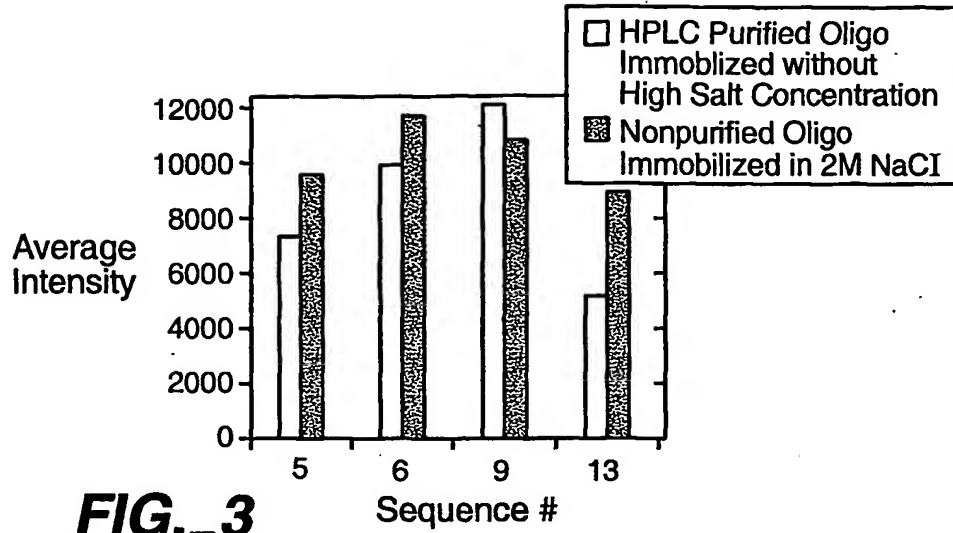
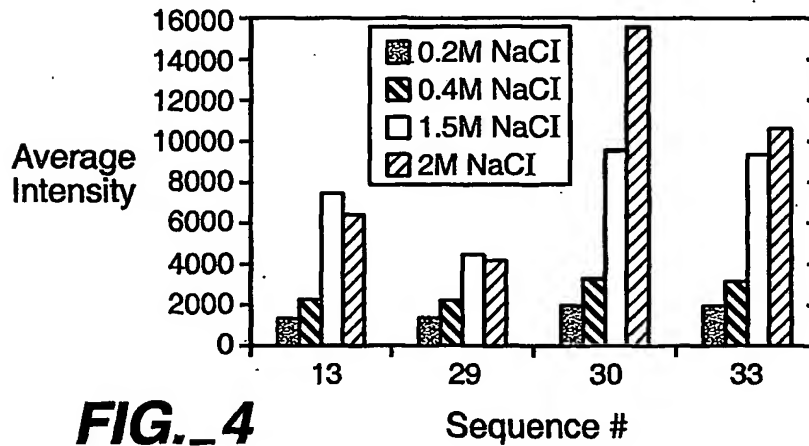
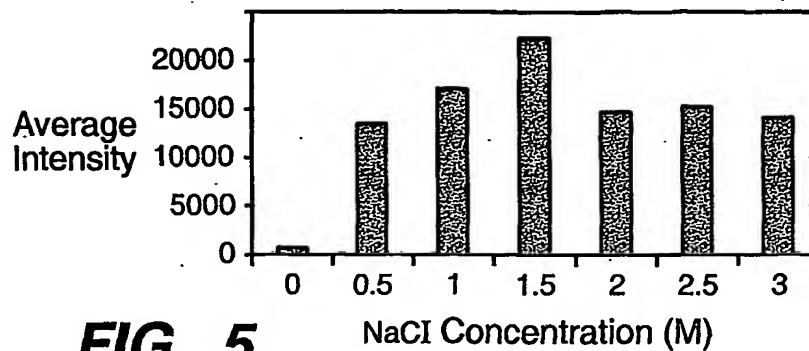
**FIG. 1**

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**Flow diagram for selection  
of probes sequences****FIG. 2**



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**FIG.\_3****FIG.\_4****FIG.\_5**